

Shears, Beverly

From: Devi, Sarvamangala
Sent: Wednesday, April 23, 2003 7:37 AM
To: Shears, Beverly
Subject: 09/711,896

Good morning Beverly:

Would you please perform a sequence and an interference search for SEQ ID NO: 1 in application SN 09/711,896?

Thanks.

S. DEVI, Ph.D.
AU 1-645
CM1-7E15

TE/2
MB

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: _____
Searcher: _____
Terminal time: 25
Elapsed time: _____
CPU time: _____
Total time: 28
Number of Searches: _____
Number of Databases: 2

Search Site

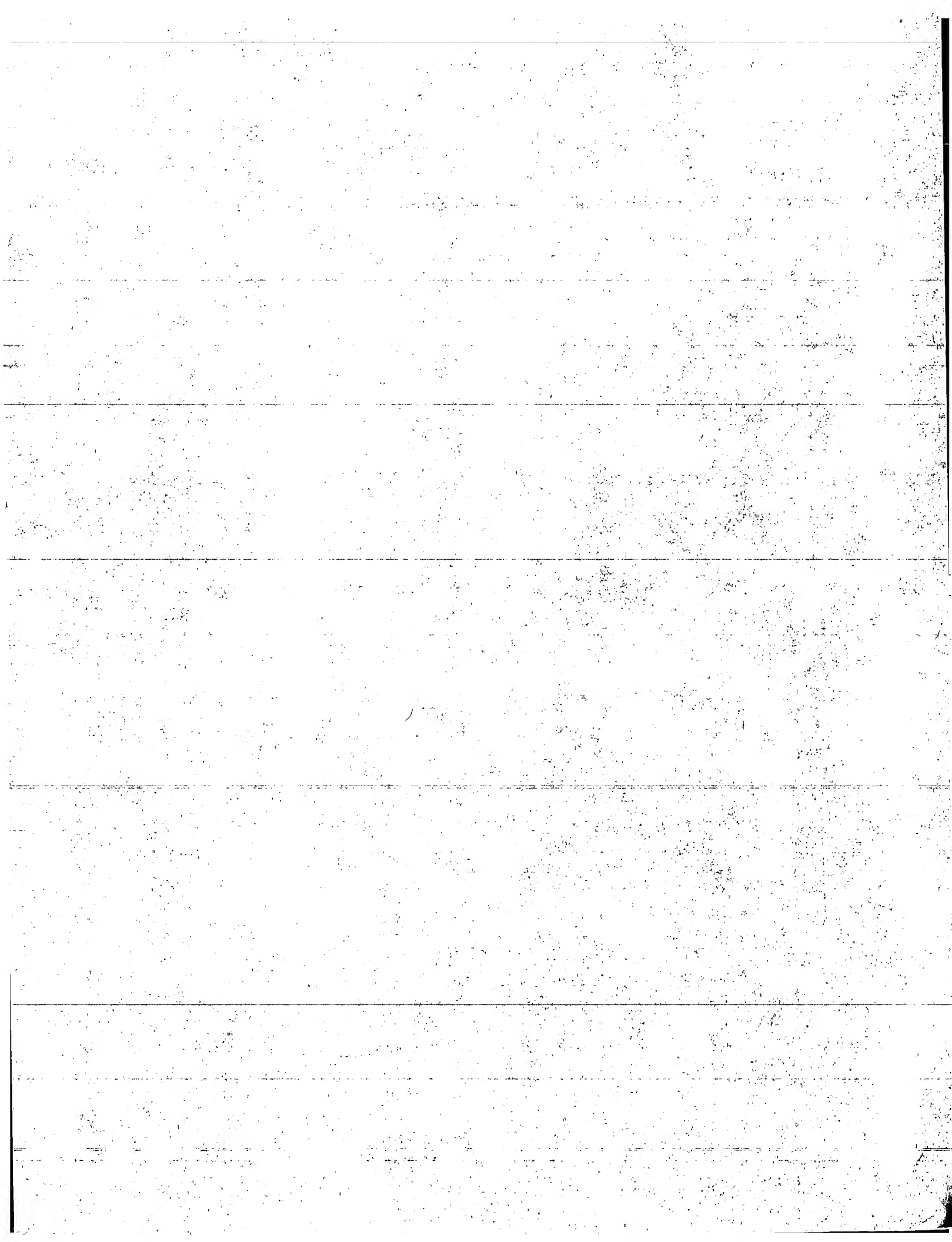
_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG Suite
_____ ☒ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ ☒ Other CGN



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:16:39 ; Search time 35 seconds
(without alignments)
137,058 Million cell updates/sec

Title: us-09-711-896a-1

Perfect score: 188

Sequence: 1 MAAEPVEDNCINEVAMKFIDNTLYFAEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5.

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	100.0	36	22 AAB82406	Human interleukin-
2	188	100.0	41	19 AAB37739	An N-terminal frag
3	188	100.0	41	19 AAW52171	Interferon-gamma i
4	188	100.0	193	17 AAR99560	Human interferon-g
5	188	100.0	193	18 AAW31757	Interferon gamma i
6	188	100.0	193	18 AAW22047	Interferon gamma i
7	188	100.0	193	19 AAW77082	Interleukin 18 act
8	188	100.0	193	19 AAW37740	Interferon-gamma i
9	188	100.0	193	19 AAW52172	Interferon-gamma i
10	188	100.0	193	19 AAW47429	Interferon-gamma p

11	188	100.0	193	19	AAW46592	Amino acid sequenc
12	188	100.0	193	21	AAV53908	Amino acid sequenc
13	188	100.0	193	22	AAB82409	Human interleukin-
14	188	100.0	193	22	AAG63830	Amino acid sequenc
15	188	100.0	193	23	AAE16953	Human precursor in
16	188	100.0	536	23	AAE16957	Human pro-IL-18/ca
17	188	100.0	588	23	AAE16958	Human pro-IL-18/ca
18	185	98.4	193	22	AAB30541	A human IL-18 with
19	179	95.2	193	22	AAV22608	Macaca cynomolgus
20	162	86.2	42	18	AAW22049	Interferon gamma i
21	159	84.6	193	21	AAV58241	Equine interleukin
22	147.5	78.5	192	22	AAG78713	Pig protein. Sus
23	147.5	78.5	192	22	AAG64653	Porcine interleukin
24	136	72.3	193	21	AAV58240	Canine interleukin
25	132	70.2	193	20	AAV01314	Canine interleukin
26	132	70.2	193	21	AAV82558	Canine interleukin
27	132	70.2	193	21	AAV82560	Canine interleukin
28	110	58.5	35	22	AAB82407	Mouse interleukin-
29	110	58.5	192	22	AAB82411	Mouse interleukin-
30	110	58.5	192	23	ABW57087	Mouse ischaemic co
31	109	58.0	175	19	AAW53283	Amino acid sequenc
32	109	58.0	194	19	AAW53282	Amino acid sequenc
33	62.5	33.2	1398	21	ABW18292	Plasmodium falcipa
34	55	29.3	274	23	ABP01892	Human ORFX protein
35	52	27.7	151	22	AAU16278	Human novel secret
36	52	27.7	156	22	ABW27680	Human peptide #331
37	52	27.7	156	22	ABW32850	Peptide #356 encod
38	52	27.7	156	22	ABW18332	Protein #331 encod
39	52	27.7	156	22	AAW66036	Human bone marrow
40	52	27.7	156	22	AAW13905	Peptide #339 encod
41	52	27.7	156	22	AAW26311	Peptide #348 encod
42	52	27.7	156	22	AAW01648	Peptide #330 encod
43	52	27.7	156	23	ABW35684	Human peptide enco
44	52	27.7	445	22	ABW30835	Peptide #3486 enco
45	52	27.7	445	22	ABW30993	Peptide #3644 enco

ALIGNMENTS

RESULT 1
AAB82406
ID AAB82406 standard; Peptide; 36 AA.
XX
AC AAB82406;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human interleukin-18 precursor propeptide sequence.
XX
KW Interleukin-18; antibody; human; infection; tumour; sarcoma;
KW autoimmune disease; therapy; diagnosis; detoxification.
XX
OS Homo sapiens.
XX
PN EP1101772-A1.
XX
PD 23-MAY-2001.
XX
PF 15-NOV-2000; 2000EP-0310121.
XX
PR 16-NOV-1999; 99JP-0324860.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Tohru K, Taniguchi M, Yamauchi H, Kurimoto M;
XX
DR WPI; 2001-368892/39.
XX
PT New antibodies specific to interleukin 18 (IL-18) precursor, useful in
PT manufacturing a medicament for treating IL-18-related diseases, e.g.
PT autoimmune disease, or for detecting, eliminating or detoxifying the
PT precursor

XX Claim 5; Page 13; 27pp; English.

XX The present sequence is that of the propeptide region of the

XX human interleukin-18 (IL-18) precursor. Monoclonal and polyclonal

XX antibodies specific to the human IL-18 precursor propeptide are

XX claimed. These are useful in detection and purification of IL-18

XX precursor, and in the elimination and detoxification of the

XX precursor accumulated in vivo. Detection methods using the

XX antibody are effective in qualitative and quantitative analyses for

XX the precursor, and also in the correction of imprecise results

XX obtained from assays using anti-IL-18 antibody, which exhibit

XX cross-reactivity against the precursor. Pharmaceutical compositions

XX comprising an antibody specific to the IL-18 precursor can be used

XX to treat viral infections including AIDS, bacterial infections,

XX solid malignant tumours, malignant tumours of haemocytes, sarcomas,

XX autoimmune disease, hepatopathy, pancreatopathy, and diseases of

XX the gallbladder, kidney and nervous system. Detection methods

XX using the antibody can be used to diagnose such diseases.

Sequence 36 AA;

Query Match 100.0%; Score 188; DB 22; Length 36;

Best Local Similarity 100.0%; Pred. No. 4.1e-21;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFIAEDDENLESD 36

Db 1 MAAPVEDNCINFVAMKFDINTLYFIAEDDENLESD 36

RESULT 2

AAW37739

ID AAW37739 standard; Protein; 41 AA.

XX AAW37739;

XX 07-JUL-1998 (first entry)

XX An N-terminal fragment of interferon-gamma inducing precursor peptide.

XX Interferon-gamma inducing precursor peptide; IFN-gamma;

XX Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;

XX antiviral agent; antitumour agent; immunopathy agent; antiseptic.

XX Mammalia.

XX EP821005-A2.

XX 28-JAN-1998.

XX 18-JUL-1997; 97EP-0305376.

XX 31-JAN-1997; 97JP-0031474.

XX 25-JUL-1996; 96JP-0213267.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kurimoto M, Tanimoto T;

XX WPI; 1998-088847/09.

XX NPSDB; AAV18906.

XX Conversion of interferon-inducing polypeptide precursor to active

XX polypeptide - comprises use of interferon-1-beta-converting enzyme,

XX useful for, e.g. enhancing cytotoxicity by killer cells

XX Claim 1; Page 14; 18pp; English.

XX This is the amino acid sequence for an N-terminal fragment of the

XX interferon-gamma (IFN-gamma) inducing precursor peptide, which is

XX cleaved to form the active mature protein when it is in contact with

XX interleukin-1-beta-converting enzyme (ICE). The polypeptide is used

CC for inducing, e.g. production of IFN-gamma a useful biologically

CC active substance, enhancing cytotoxicity by, and inducing the

CC formation of killer cells. The polypeptide may potentially be used

CC as an antiviral, antitumour and immunopathy agent and as an antiseptic.

XX Sequence 41 AA;

Query Match 100.0%; Score 188; DB 19; Length 41;

Best Local Similarity 100.0%; Pred. No. 4.8e-21;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFIAEDDENLESD 36

Db 1 MAAPVEDNCINFVAMKFDINTLYFIAEDDENLESD 36

RESULT 3

AAW52171

ID AAW52171 standard; peptide; 41 AA.

XX AAW52171;

XX 10-JUN-1998 (first entry)

XX Interferon-gamma inducing polypeptide precursor N-terminal fragment.

XX Interferon-gamma; IFN-gamma; precursor; enzyme; cleavage.

XX Homo sapiens

XX Key Location/Qualifiers

XX Cleavage-site 36..37 "an enzyme cleaves the linkage between Asp

XX and Tyr to convert the precursor into its

XX active form"

XX EP819757-A2.

XX 21-JAN-1998

XX 18-JUL-1997; 97EP-0305377.

XX 30-MAY-1997; 97JP-0156062.

XX 19-JUL-1996; 96JP-0207691.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kurimoto M, Tanimoto T;

XX WPI; 1998-078838/08.

XX Polypeptide-processing enzyme - for preparing mature form of

XX interferon-inducing polypeptide

XX Claim 2; Page 14; 18pp; English.

XX This is the N-terminal fragment of a precursor of an interferon-gamma

XX (IFN-gamma) inducing polypeptide. The polypeptide induces IFN-gamma

XX production in immunocompetent cells [the polypeptide is not named but

XX is described in JP 27198/96 and 193098/96]. An enzyme can convert the

XX precursor form into its active form by cleaving a linkage between Asp

XX at amino acid position 36 and Tyr at amino acid position 37 of this

XX fragment. The enzyme can be obtained from a human haematopoietic cell

XX and can be inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-

XX alanyl-L-aspartyl-L-al. The enzyme can be used for cleaving a recombinant

XX IFN-gamma pro-polypeptide to form a mature polypeptide.

XX Sequence 41 AA;

Query Match 100.0%; Score 188; DB 19; Length 41;

Best Local Similarity 100.0%; Pred. No. 4.8e-21;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36
 |||
 Db 1 MAAPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36

RESULT 4

AAAR99560
 ID AAR99560 standard; Protein; 193 AA.

XX AC AAR99560;

XX DT 29-SEP-1996 (first entry)

XX DE Human interferon-gamma inducer protein.

XX KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
 KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
 KW therapy; cancer.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..36

XX FT Protein /label= Leader_peptide

XX FT Misc-difference 109

XX FT /label= Mat_protein

XX FT /label= Ile, Thr

XX PN EP712931-A2.

XX XX 22-MAY-1996.

XX PD 10-NOV-1995; 95EP-0308055.

XX PF 29-SEP-1995; 95JP-0274988.

XX PR 15-NOV-1994; 94JP-0304203.

XX PR 23-FEB-1995; 95JP-0058240.

XX PR 10-MAR-1995; 95JP-0078357.

XX PR 18-SEP-1995; 95JP-0262062.

XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX PI Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;

XX PI Taniguchi M, Tanimoto T, Torigoe K, Ushio S;

XX DR WPI; 1996-252837/26.

XX DR N-PSDB; AAT32404.

XX FT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful

XX FT to treat and prevent, e.g. viral disease, malignancies and immune

XX FT disorders

XX PS Claim 6; Page 41-42; 48pp; English.

XX CC The mature portion of a novel human protein, (AAR99560) induces

XX CC interferon-gamma (IFN-gamma) prodn. by immunocompetent cells. It

XX CC is the product of a cDNA clone (AAT32404) obtd. from a human liver

XX CC library. The protein enhances the cytotoxicity of killer cells

XX CC and/or induces the formation of killer cells (e.g. NK cells,

XX CC lymphokine-activating killer (LAK) cells, and cytotoxic T-cells).

XX CC The mature protein (see also AAR99558) is useful as an antiviral,

XX CC antitumor, antibacterial, immunoregulatory and blood platelet

XX CC enhancing agent, and can be used in adoptive immunotherapy. It is

XX CC also used to raise monoclonal antibodies.

XX XX Sequence 193 AA;

XX Query Match 100.0%; Score 188; DB 17; Length 193;

XX Best Local Similarity 100.0%; Pred. No. 3e-20;

XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36

Db 1 MAAPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36
 |||
 Db 1 MAAPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36

RESULT 5

AAW31757
 ID AAW31757 standard; Protein; 193 AA.

XX AC AAW31757;

XX DT 15-JAN-1998 (first entry)

XX DE Interferon gamma inducing factor-2 (IGIF-2) R140I variant.

XX KW Interferon gamma inducing factor-2; IGIF-2; leucocyte; lymphocyte; human;
 KW inflammation; proliferation; differentiation; maturation; tissue damage.

XX OS Homo sapiens;

XX FH Key Location/Qualifiers

XX FT Misc-difference 140

XX FT /label= R140I

XX FT /note= "Wild type Arg is replaced by Ile"

XX PN WO9724441-A1.

XX PD 10-JUL-1997.

XX PF 20-DEC-1996; 96WO-US20432.

XX PR 29-DEC-1995; 95US-0580667.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Cocks BG, Coleman R, Hawkins PR;

XX DR WPI; 1997-363677/33.

XX DR N-PSDB; AAT74988.

XX PT Novel interferon gamma inducing factor-2 - used to screen for

XX PT compounds to diagnose, treat or prevent tissue damage associated

XX PT with inflammation

XX PS Claim 3; Page -; 60pp; English.

XX CC This protein sequence represents an interferon gamma inducing factor-2

XX CC (IGIF-2) variant, identified from a liver cDNA library. This sequence

XX CC differs from IGIF-2 identified from a T-lymphocyte cDNA library

XX CC (AAW22047), in that amino acid 140 is found to be changed from Arg to

XX CC Ile. A second variant, AAW22049, also exists. Probes derived from the

XX CC nucleic acid sequences can be used to quantify the expression of IGIF-2

XX CC in conditions that are associated with inflammation or aberrant

XX CC expression of IGIF-2. The protein can be used to screen for compounds

XX CC that interact with IGIF-2, such as antibodies, antagonists or other

XX CC inhibitors (especially ribozymes or antisense sequences) of IGIF-2

XX CC expression or activity. The protein can also be used to diagnose, prevent

XX CC or treat IGIF-2 induction of proliferation, differentiation or maturation

XX CC of leucocytes or lymphocytes, especially in relation to tissue damage

XX CC associated with inflammation.

XX CC Note:- This sequence does not appear in the specification; it has

XX CC been made by modifying the IGIF-2 sequence presented in AAW22047.

XX XX Sequence 193 AA;

XX Query Match 100.0%; Score 188; DB 18; Length 193;

XX Best Local Similarity 100.0%; Pred. No. 3e-20;

XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36

Db 1 MAAPVEDNCINFVAMKFDINTLYFTAEDDENLESD 36

RESULT 6
AAW22047
ID AAW22047 standard; Protein: 193 AA.
XX
AC AAW22047;
XX
DT 14-JAN-1998 (first entry)
XX
DE Interferon gamma inducing factor-2 (IGIF-2) protein.
XX
KW Interferon gamma inducing factor-2; IGIF-2; leucocyte; lymphocyte;
KW inflammation; proliferation; differentiation; maturation; tissue damage;
KW human.
XX
OS Homo sapiens.
XX
PN WO9724441-A1.
XX
XX 10-JUL-1997.
XX
XX 20-DEC-1996; 96WO-US20432.
XX
XX 29-DEC-1995; 95US-0580667.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Cocks BG, Coleman R, Hawkins PR;
XX
XX WPI; 1997-363677/33.
XX
XX N-PSDB; AAT74987.
XX
XX Novel interferon gamma inducing factor-2 - used to screen for
XX compounds to diagnose, treat or prevent tissue damage associated
XX with inflammation
XX
XX Claim 1; Page 46; 60pp; English.
XX
XX This is the protein sequence of interferon gamma inducing factor-2
XX (IGIF-2). An IGIF-2 variant (AAW31157) and an IGIF variant (AAW22049),
XX which may be an alternate transcript, also exist. Probes derived from
XX the nucleic acid sequences can be used to quantify the expression of
XX IGIF-2 in conditions that are associated with inflammation or aberrant
XX expression of IGIF-2. The protein can be used to screen for compounds
XX that interact with IGIF-2, such as antibodies, antagonists or other
XX inhibitors (especially ribozymes or antisense sequences) of IGIF-2
XX expression or activity. The protein can also be used to diagnose,
XX prevent or treat IGIF-2 induction of proliferation, differentiation or
XX maturation of leucocytes or lymphocytes, especially in relation to tissue
XX damage associated with inflammation.
XX
XX
XX Sequence 193 AA;
XX
XX Query Match 100.0%; Score 188; DB 18; Length 193;
XX Best Local Similarity 100.0%; Pred. No. 3e-20;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX
XX
XX RESULT 7
AAW77082
ID AAW77082 standard; Protein: 193 AA.
XX
AC AAW77082;
XX
XX 16-NOV-1998 (first entry)
XX
XX Interleukin 18 active protein and precursor.
XX
XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
XX osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
XX

Chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
Homo sapiens.
Key Location/Qualifiers
Peptide 1..36: "Signal peptide"
Peptide 37..193
Peptide /note= "Mature peptide"
XX
XX EP861663-A2.
XX
XX 02-SEP-1998.
XX
XX 24-FEB-1998; 98EP-0301352.
XX
XX 25-FEB-1997; 97JP-0055468.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX
XX WPI; 1998-448964/39.
XX
XX N-PSDB; V4828.
XX
XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
XX osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
XX primary hyperthyroidism and osteoporosis
XX
XX Disclosure; Page 24-28; 56pp; English.
XX
XX Interleukin-18 (IL-18) or a functional equivalent can be used for
XX inhibition of osteoclast formation. IL-18 is used for treating or
XX preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
XX Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
XX arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
XX osteoporosis.
XX
XX -Sequence 193 AA;
XX
XX Query Match 100.0%; Score 188; DB 19; Length 193;
XX Best Local Similarity 100.0%; Pred. No. 3e-20;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX
XX
XX RESULT 8
AAW37740
ID AAW37740 standard; Protein: 193 AA.
XX
AC AAW37740;
XX
XX 07-JUL-1998 (first entry)
XX
XX Interferon-gamma inducing precursor peptide.
XX
XX Interferon-gamma inducing precursor peptide; IFN-gamma;
XX interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
XX antiviral agent; antitumour agent; immunopathy agent; antiseptic.
XX
XX Mammalia.
XX
XX Key Location/Qualifiers
XX Protein 36..157
XX /note= "Mature protein"
XX Misc-difference 109
XX /label= Ile, Thr
XX
XX Cleavage-site 36..37
XX

DR WPI: 1998-078838/08.
DR N-PSDB; AAVI7200.

XX
XX
PT Polypeptide-processing enzyme - for preparing mature form of
PT interferon-inducing polypeptide

XX
XX Claim 3: Page 15; 18pp; English.

XX This sequence represents the precursor of an interferon-gamma (IFN-gamma) inducing polypeptide. The polypeptide induces IFN-gamma production in immunocompetent cells [the polypeptide is not named but is described in JP 27198/96 and 193098/96]. An enzyme can convert this precursor form into its active form by cleaving a linkage between Asp at amino acid position 36 and Tyr at amino acid position 37 of its N-terminal fragment. The enzyme can be obtained from a human haematopoietic cell and can be inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-aspart-L-al. The enzyme can be used for cleaving a recombinant IFN-gamma pro-polypeptide to form a mature polypeptide.

XX Sequence 193 AA;
SQ

Query Match 100.0%; Score 188; DB 19; Length 193;
Best Local Similarity 100.0%; Pred. No. 3e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAEPVEDNCINFAVKFIDNTLYFIAEDDNELESD 36
| | | | | | | | | | | | | | | | | |
DB 1 MAEPVEDNCINFAVKFIDNTLYFIAEDDNELESD 36

RESULT 10
AAW47429

ID AAW47429 standard; Protein; 193 AA.
XX AC AAW47429;
XX DT 05-JUN-1998 (first entry)
XX Interferon-gamma production inducer.
KW Interferon-gamma; IFN-gamma; production inducer; gene therapy;
KW immunocompetent-cell; treatment; prevention; malignant-tumour;
KW viral infection; bacterial infection; immune disease.
XX Homo sapiens.
OS
XX Location/Qualifiers
FH Peptide 1..36
FT /label= sig_peptide
FT Peptide 37..193
FT /label= mat_peptide
FT Misc-difference 109
FT /label= Ile, Thr
XX
XX EP816499-A2.
XX PN
XX PD 07-JAN-1998.
XX
XX 27-JUN-1997; 97EP-0304616.
XX
XX 27-JUN-1996; 96JP-0185305.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX Kurimoto M, Okura T, Torigoe K;
XX WPI: 1998-054914/06.
XX N-PSDB; AAV15825, AAV15826.
XX Genomic DNA encoding polypeptide inducing interferon-gamma
XX production - by immuno-competent cells, useful to treat e.g. human
XX malignant tumours or viral diseases
XX PT
XX PT
XX PT

PS Claim 2; Pages 49-50; 74pp; English.

CC The present sequence is a protein, which induces

CC interferon-gamma (IFN-gamma) production in immunocompetent cells.

CC The protein has high biological activity, including enhancing

CC cytotoxicity of killer cells and inducing killer cell formation,

CC in addition to inducing IFN-gamma production by immunocompetent

CC cells when expressed in mammalian cells, facilitating its use in

CC low dosages to treat/prevent, e.g. malignant tumours, viral or

CC bacterial infections and immune diseases. As it is expressed in

CC mammalian cells, it also has low toxicity when used in human

CC treatments, minimising side effects. The DNA encoding the protein

CC can be used in gene therapy, e.g. by infecting vectors containing

CC the DNA or transplanting cells.

XX

SQ Sequence 193 AA;

Query Match 100.0%; Score 188; DB 19; Length 193;

Best Local Similarity 100.0%; Pred. No. 3e-20;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

|||||

Db 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

|||||

RESULT 11

AAW46592

ID AAW46592 standard; Protein: 193 AA.

XX

AC AAW46592;

XX

XX 21-MAY-1998 (first entry)

DT

DE Amino acid sequence of human interleukin-1-gamma.

XX

KW Interleukin-1-gamma; IL-1-gamma; mouse; cytokine; IGIF; interferon-gamma;

KW induction; antibody; diagnostic assay; fusion protein; activity;

KW immunological disorder; allergy.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Region 41..47 "beta-1 region"

FT /note= "beta-1 region"

FT Region 55..59 "beta-2 region"

FT /note= "beta-2 region"

FT Region 64..68 "beta-3 region"

FT /note= "beta-3 region"

FT Region 83..88 "beta-4 region"

FT /note= "beta-4 region"

FT Region 96..102 "beta-5 region"

FT /note= "beta-5 region"

FT Region 108..113 "beta-6 region"

FT /note= "beta-6 region"

FT Region 115..120 "beta-7 region"

FT /note= "beta-7 region"

FT Region 137..143 "beta-8 region"

FT /note= "beta-8 region"

FT Region 147..153 "beta-9 region"

FT /note= "beta-9 region"

FT Region 160..164 "beta-10 region"

FT /note= "beta-10 region"

FT Region 170..175 "beta-11 region"

FT /note= "beta-11 region"

FT Region 187..191 "beta-12 region"

FT /note= "beta-12 region"

XX

XX W09744468-A1.

XX

PD 27-NOV-1997.

XX

PF 16-MAY-1997; 97WO-US07282.

XX

20-MAY-1996; 96US-0651998.

XX

PA (SCHE) SCHERING CORP.

XX

PI Bazan JF; Hardiman GT; Kastelein RA; Sana TR; Timans JC;

XX

DR WPI; 1998-018522/02.

DR N-PSDB; AAV05368.

XX

PT Antagonist of human interleukin-1-gamma - used for treating

PT immunological disorders caused by human IL-1-gamma.

XX

PS Disclosure; Pages 54-55; 63pp; English.

XX

CC The present sequence represents human interleukin-1-gamma (IL-1-gamma).

CC The protein is the human equivalent of a mouse cytokine, IGIF, which

CC induces certain T cells to produce interferon-gamma. Human IL-1-gamma

CC and mouse IGIF show 71% identity at the nucleotide level and

CC approximately 65% identity at the amino acid level. Antagonists of

CC IL-1 gamma, e.g. antibodies, can be used in a method for treating a

CC condition caused by human IL-1 gamma. The antibodies can also be used

CC in diagnostic assays. The IL-1-gamma protein can be covalently fused

CC conjugated to polyethylene glycol or to a polypeptide, and the fusion

CC protein used in a pharmaceutical composition for supplying the

CC biological activity of IL-1 gamma. Conditions that can be treated using

CC the human IL-1-gamma protein include immunological disorders, allergies,

CC and infectious diseases. The IL-1-gamma can also be used to detect the

CC presence of the protein or its receptor.

XX

SQ Sequence 193 AA;

Query Match 100.0%; Score 188; DB 19; Length 193;

Best Local Similarity 100.0%; Pred. No. 3e-20;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

|||||

Db 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

|||||

RESULT 12

AAV53908

ID AAV53908 standard; Protein: 193 AA.

XX

AC AAV53908;

XX

XX 13-MAR-2000 (first entry)

DT

DE Amino acid sequence of a protein that induces IFN-gamma production.

XX

KW Human; interferon gamma production; IFN-gamma; immunocompetent cell;

KW antiviral; immunoregulatory; antigen; mitogen;

KW IFN-gamma susceptible disease; antibacterial; antitumour;

KW blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;

KW AIDS; bacterial disease; Candidiasis; malaria; solid malignant tumour;

KW renal cancer; mycosis; fungoides; chronic granulomatous disease;

KW blood cell malignant tumour; adult T cell leukaemia;

KW chronic myelogenous leukaemia; malignant leukaemia; immune disease

KW allergy; rheumatism.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Peptide 1..36

FT /note= "signal peptide"

FT Protein 37..193

FT /note= "mature protein"

FT Misc-difference 109

FT /label= Ile, Thr

FT /note= "encoded by AYT"

XX

XX EP962531-A2.

XX PD 08-DEC-1999.
 XX PF 10-NOV-1995; 99EP-0104104.
 XX PR 15-NOV-1994; 94JP-0304203.
 XX PR 23-FEB-1995; 95JP-0058240.
 XX PR 10-MAR-1995; 95JP-0078357.
 XX PR 18-SEP-1995; 95JP-0262062.
 XX PR 29-SEP-1995; 95JP-0274988.
 XX PR 10-NOV-1995; 95EP-0308055.
 XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX PI Ushio S, Torigoe K, Tanimoto T, Okamura H;
 XX DR WPI; 2000-064289/06.
 XX DR N-PSDB; AAZ36876.
 XX PT Novel polypeptides used in the treatment of interferon-gamma
 XX PT susceptible diseases
 XX PS Example A-4-3; Page 7; 42pp; English.
 XX CC The present sequence represents a human protein that induces interferon
 CC (IFN)-gamma production by immunocompetent cells. IFN-gamma is a
 CC protein which has antiviral, antioncotic and immunoregulatory activities,
 CC and is produced by immunocompetent cells stimulated with antigens or
 CC mitogens. The protein of the invention is used to treat IFN-gamma
 CC susceptible diseases, and also have use as a antiviral agent,
 CC antibacterial agent, antitumour agent, immunoregulatory agent and blood
 CC platelet enhancing agent. Diseases which can be treated with the
 CC protein include viral diseases such as hepatitis, herpes syndrome,
 CC condyloma, and AIDS; bacterial diseases such as Candidiasis and
 CC malaria; solid malignant tumours such as renal cancer, mycosis
 CC fungoides, and chronic granulomatous disease; blood cell malignant
 CC tumours such as adult T cell leukaemia, chronic myelogenous leukaemia,
 CC and malignant leukaemia; and immune diseases such as allergy and
 XX rheumatism.
 XX SQ Sequence 193 AA;
 Query Match 100.0%; Score 188; DB 21; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFAVAMKFDINTLYFAEDDENLESD 36
 ||||||||||||||||||||||||||||||||||||
 DB 1 MAAPVEDNCINFAVAMKFDINTLYFAEDDENLESD 36
 RESULT 13
 AAB82409
 ID AAB82409 standard; Protein; 193 AA.
 XX AC AAB82409;
 XX DT 06-AUG-2001 (first entry)
 XX DE Human interleukin-18 precursor.
 XX KW Interleukin-18; antibody; human; infection; tumour; sarcoma;
 KW autoimmune disease; therapy; diagnosis; detoxification.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Peptide 1..36
 XX FT Protein /label= Signal_peptide
 XX FT /label= Mature_protein
 XX FT Misc-difference 109
 XX FT /label= Ile, Thr

XX EP1101772-A1.
 XX PD 23-MAY-2001.
 XX PF 15-NOV-2000; 2000EP-0310121.
 XX PR 16-NOV-1999; 99JP-0324860.
 XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX PI Tohru K, Taniguchi M, Yamauchi H, Kurimoto M;
 XX DR WPI; 2001-368892/39.
 XX DR N-PSDB; AAF90444.
 XX PT New antibodies specific to interleukin 18 (IL-18) precursor, useful in
 XX PT manufacturing a medicament for treating IL-18-related diseases, e.g.
 XX PT autoimmune disease, or for detecting, eliminating or detoxifying the
 XX PT precursor
 XX PS Example 1-2; Page 14-15; 27pp; English.
 XX CC The present sequence is that of human interleukin-18 (IL-18)
 CC precursor. Monoclonal and polyclonal antibodies specific
 CC to the human IL-18 precursor propeptide (see AAB82406) are
 CC claimed. These are useful in detection and purification of IL-18
 CC precursor, and in the elimination and detoxification of the
 CC precursor accumulated in vivo. Detection methods using the
 CC antibody are effective in qualitative and quantitative analyses for
 CC the precursor, and also in the correction of imprecise results
 CC obtained from assays using anti-IL-18 antibody, which exhibit
 CC cross-reactivity against the precursor. Pharmaceutical compositions
 CC comprising an antibody specific to the IL-18 precursor can be used
 CC to treat viral infections including AIDS, bacterial infections,
 CC solid malignant tumours, malignant tumours of haemocytes, sarcomas,
 CC autoimmune disease, hepatopathy, pancreatopathy, and diseases of
 CC the gallbladder, kidney and nervous system. Detection methods
 CC using the antibody can be used to diagnose such diseases.
 XX SQ Sequence 193 AA;
 Query Match 100.0%; Score 188; DB 22; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFAVAMKFDINTLYFAEDDENLESD 36
 ||||||||||||||||||||||||||||||||||||
 DB 1 MAAPVEDNCINFAVAMKFDINTLYFAEDDENLESD 36
 RESULT 14
 AAG63830
 ID AAG63830 standard; Protein; 193 AA.
 XX AC AAG63830;
 XX DT 26-NOV-2001 (first entry)
 XX DE Amino acid sequence of human interleukin 18 (IL-18).
 XX KW T-cell-helper type 2 response; Th2 response; T cell mediated response;
 KW allergic response; interleukin 18; IL-18; IGE-mediated allergy;
 KW allergic asthma; anaphylactic reaction; asthma associated allergy;
 KW IGE dependent allergic rhinoconjunctivitis.
 XX OS Homo sapiens.
 XX PN WO200168896-A1.
 XX PD 20-SEP-2001.
 XX PF 02-MAR-2001; 2001WO-US06869.

XX 10-MAR-2000; 2000US-0188311.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Levy S, Dekruyff RH, Umetsu DT, Maecker H;
 XX WPI; 2001-570874/64.
 XX N-PSDB; AAH78060.
 XX
 XX Reducing antigen specific immune response in conditions such as asthma,
 XX allergic rhinitis, by reducing a T-cell-helper type 2 T cell mediated
 XX antigen-specific allergic response
 XX
 XX Disclosure; Page 36; 38pp; English.
 XX
 XX The specification describes a method for reducing a T-cell-helper
 XX type 2 (Th2) T cell mediated antigen-specific allergic response. The
 XX method comprises administering a DNA construct encoding a fusion
 XX protein of interleukin 18 (IL-18) and an antigen associated with the
 XX allergic response. The method is useful for reducing a Th2 T cell
 XX mediated antigen-specific allergic response especially IgE-mediated
 XX allergic asthma or anaphylactic reactions or IgE dependent allergic
 XX rhinoconjunctivitis, and for treating asthma associated allergies where
 XX the allergies are ongoing at the time of the administration. The
 XX present sequence represents a human IL-18, and is used to construct
 XX fusion proteins of the invention.
 XX
 XX Sequence 193 AA;
 SQ
 Query Match 100.0%; Score 188; DB 22; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3e-20; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 0;
 QY 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
 Db 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
 RESULT 15
 AAEL6953
 ID AAE16953 standard; Protein; 193 AA.
 XX
 XX AAE16953;
 XX
 XX 18-APR-2002 (first entry)
 XX
 XX Human precursor interleukin-18 (Pro-IL-18) protein.
 KW Human; precursor interleukin-18; pro-IL-18; caspase; interferon gamma;
 KW IFN-gamma; immunocompetent.
 XX Homo sapiens.
 OS
 XX WO200198455-A2.
 XX
 XX 27-DEC-2001.
 PD
 XX
 XX 11-JUN-2001; 2001WO-US18804.
 XX
 XX 15-JUN-2000; 2000US-211832P.
 PR
 XX 10-AUG-2000; 2000US-224128P.
 PR
 XX 20-JAN-2001; 2001US-264923P.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX Johanson KO, Kirkpatrick RB, Shatzman AR, Ho YS, Mcdevitt P;
 PI
 XX WPI; 2002-139786/18.
 DR
 XX N-PSDB; AAD27364.
 DR
 XX Activation of precursor polypeptide e.g. interleukin-18 polypeptide
 PT useful for inducing interferon-gamma production, comprises contacting

PT or co-expressing caspase 4 or caspase 5 with precursor polypeptide
 XX Claim 7; Fig 1; 64pp; English.
 PS
 XX The invention relates to a method for the in vitro activation of human
 CC precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The
 CC method comprises contacting precursor IL-18 with an activating enzyme
 CC such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family
 CC of cysteine proteases that include interleukin-1beta converting enzyme
 CC (ICE), which preferentially cleave substrates containing a protease
 CC activation motif. The methods are useful for producing physiologically
 CC active polypeptide e.g. active IL-18 polypeptide. The active IL-18
 CC polypeptide has an activity of inducing the production of interferon
 CC (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a
 CC biologically active substance for stimulating the production of IFN-g
 CC from KG-1 (human myelomonocytic cell line) cells. The present sequence
 CC is human Pro-IL-18 protein.
 XX
 XX Sequence 193 AA;
 SQ
 Query Match 100.0%; Score 188; DB 23; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3e-20; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 0;
 QY 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
 Db 1 MAAPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
 Search completed: April 23, 2003, 08:19:47
 Job time : 36 secs

GenCore version 5.1.4.p5 4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:16:39 : Search time 29 seconds
(without alignments)
36.525 Million cell updates/sec

Title: us-09-711-896A-1

Perfect score: 188

Sequence: 1 MAAPVEDNCINFVAMKFDNTLYIAEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	100.0	41	2	US-08-896-605A-1
2	188	100.0	41	2	US-08-896-501A-1
3	188	100.0	193	2	US-08-896-605A-2
4	188	100.0	193	2	US-08-896-501A-2
5	188	100.0	193	4	US-08-832-180-9
6	179	95.2	193	4	US-09-597-576-2
7	50	26.6	536	4	US-08-653-648A-13
8	49	26.1	747	3	US-08-089-397A-16
9	49	26.1	776	1	US-07-603-133B-17
10	49	26.1	776	1	US-07-603-133B-20
11	49	26.1	776	3	US-08-089-397A-15
12	48.5	25.8	464	1	US-07-991-867B-2
13	48.5	25.8	464	1	US-08-107-755A-2
14	48.5	25.8	464	2	US-08-544-332-2
15	48.5	25.8	464	2	US-09-370-861A-2
16	48	25.5	688	4	US-09-113-750A-3
17	47	25.0	475	4	US-09-212-247C-4
18	47	25.0	694	2	US-08-895-522-4
19	47	25.0	694	3	US-09-195-391-4
20	47	25.0	775	1	US-07-603-133B-15
21	47	25.0	775	1	US-07-603-133B-16
22	46	24.5	266	4	US-09-414-276-8
23	46	24.5	1170	2	US-08-789-078-2
24	46	24.5	1170	2	US-08-752-633-2
25	46	24.5	1170	2	US-08-476-062A-42
26	46	24.5	1170	5	PCT-US95-04886-2
27	46	24.5	1170	5	PCT-US96-01314-42

28	46	24.5	2409	6	5180808-2	Patent No. 5180808
29	45	23.9	322	4	US-09-080-205-8	Sequence 8, Appli
30	45	23.9	365	2	US-08-204-288-7	Sequence 7, Appli
31	45	23.9	395	4	US-09-134-001C-5119	Sequence 5119, Ap
32	45	23.9	906	1	US-08-486-270-2	Sequence 2, Appli
33	45	23.9	906	3	US-08-367-264-2	Sequence 2, Appli
34	45	23.9	906	4	US-09-153-757-2	Sequence 2, Appli
35	45	23.9	906	5	PCT-US91-09422-17	Sequence 17, Appli
36	45	23.9	1056	2	US-08-687-289A-7	Sequence 7, Appli
37	45	23.9	1056	2	US-08-687-289A-8	Sequence 8, Appli
38	45	23.9	1058	2	US-08-687-289A-5	Sequence 5, Appli
39	45	23.9	1194	4	US-08-538-526-1	Sequence 1, Appli
40	45	23.9	1199	1	US-08-041-538-2	Sequence 2, Appli
41	45	23.9	1199	1	US-08-463-642-2	Sequence 2, Appli
42	45	23.9	1199	1	US-08-455-602-2	Sequence 2, Appli
43	45	23.9	1199	2	US-08-465-157-2	Sequence 2, Appli
44	45	23.9	1199	5	PCT-US91-09422-2	Sequence 2, Appli
45	44.5	23.7	137	4	US-09-134-001C-4731	Sequence 4731, Ap

ALIGNMENTS

RESULT 1
US-08-896-605A-1
; Sequence 1, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 July 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal fragment
; US-08-896-605A-1

Query Match 100.0%; Score 188; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
Db 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

RESULT 2
US-08-896-501A-1
; Sequence 1, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO=3
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: N-terminal fragment

US-08-896-501A-1
Query Match 100.0%; Score 188; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
Db 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

RESULT 3
US-08-896-605A-2
; Sequence 2, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997

US-08-896-605A-2
Query Match 100.0%; Score 188; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.6e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
Db 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

RESULT 4
US-08-896-501A-2
; Sequence 2, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 July 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO=2
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-896-605A-2
Query Match 100.0%; Score 188; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
Db 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

RESULT 4
US-08-896-501A-2
; Sequence 2, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997

US-08-896-501A-2
Query Match 100.0%; Score 188; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
Db 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

RESULT 4
US-08-896-501A-2
; Sequence 2, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997

US-08-896-501A-2
Query Match 100.0%; Score 188; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36
Db 1 MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD 36

RESULT 4
US-08-896-501A-2
; Sequence 2, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997

;; FILING DATE: 31-JAN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: TANIMOTO-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 193 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-896-501A-2

Query Match 100.0%; Score 188; DB:2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MAAEPVEDNCINFVAMKFDINTLYFTAEADENLESD 36
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Db 1 MAAEPVEDNCINFVAMKFDINTLYFTAEADENLESD 36

RESULT 5

US-08-832-180-9
; Sequence 9, Application US/08832180
; Patent No. 6214584
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: USHIO, Shimei
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: OKAMURA, Haruki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,180
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,191
; FILING DATE:
; APPLICATION NUMBER: JP 304,203/94
; FILING DATE: No. 6214584member 15, 1994
; APPLICATION NUMBER: 10048102
; FILING DATE: September 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: USHIO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 193 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-832-180-9

Query Match 100.0%; Score 188; DB:4; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFTAEADENLESD 36
|||||
Db 1 MAAEPVEDNCINFVAMKFDINTLYFTAEADENLESD 36

RESULT 6

US-09-597-576-2
; Sequence 2, Application US/09597576
; Patent No. 6432678
; GENERAL INFORMATION:
; APPLICANT: Alexander Taylor
; APPLICANT: Han Trinh
; TITLE OF INVENTION: MACACA CYNOMOLGUS IL18
; FILE REFERENCE: GP-70629
; CURRENT APPLICATION NUMBER: US/09/597,576
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/140,140
; PRIOR FILING DATE: 1999-06-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2:
; LENGTH: 193
; TYPE: PRT
; ORGANISM: MACACA CYNOMOLGUS
US-09-597-576-2

Query Match 95.2%; Score 179; DB:4; Length 193;
Best Local Similarity 94.4%; Pred. No. 2.3e-19;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFTAEADENLESD 36
|||||
Db 1 MAAEPVEDNCINFVAMKFDINTLYFTAEADENLESD 36

RESULT 7

US-08-653-648A-13
; Sequence 13, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/JUS
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Chironomus tentans
US-08-653-648A-13

REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-603-133B-20

Query Match 26.1%; Score 49; DB 1; Length 776;
Best Local Similarity 52.6%; Pred. No. 38;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 17 KFDINTLYFIAEDDENLES 35
||| | | : ||| | |
Db 666 KFIPNRYRVIKDEVLEA 684

RESULT 11
US-08-089-397A-15
Sequence 15, Application US/08089397A
Patent No. 6086880
GENERAL INFORMATION:
APPLICANT: SABARA, MARTA I. J.
APPLICANT: FRENCHICK, PATRICK J.
APPLICANT: POTTER, ANDREW A.
APPLICANT: IJAZ, MOHAMMAD K.
APPLICANT: GILCHRIST, JAMES E.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ROTAVIRUS VACCINES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 530
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 29311-20003.03
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-089-397A-15

Query Match 26.1%; Score 49; DB 3; Length 776;
Best Local Similarity 52.6%; Pred. No. 38;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 17 KFDINTLYFIAEDDENLES 35

Db 666 KFIPNRYRVIKDEVLEA 684
||| | | : ||| | |

RESULT 12
US-07-991-867B-2
Sequence 2, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C3
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-991-867B-2

Query Match 25.8%; Score 48.5; DB 1; Length 464;
Best Local Similarity 57.9%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INEVAMKF---IDNTLYFI 26
||| | | : ||| | |

Db 20 INFMSMLFFSKIDNMVYFI 38
||| | | : ||| | |
RESULT 13
US-08-107-755A-2
Sequence 2, Application US/08107755A
Patent No. 5721352
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UFI14.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-755A-2

Query Match 25.8%; Score 48.5; DB 1; Length 464;
Best Local Similarity 57.9%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKF---IDNTLYFI 26
Db 20 INFMSMLFFSKIDNMYFI 38

RESULT 14
US-08-544-332-2
Sequence 2, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UFI14.C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-544-332-2

Query Match 25.8%; Score 48.5; DB 2; Length 464;
Best Local Similarity 57.9%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKF---IDNTLYFI 26
Db 20 INFMSMLFFSKIDNMYFI 38

RESULT 15
US-09-370-861A-2
Sequence 2, Application US/09370861A
Patent No. 6410221
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No.16410221el Entomopoxvirus Expression System
FILE REFERENCE: UFI14.C4.D1
CURRENT APPLICATION NUMBER: US/09/370,861A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 07/991,867
PRIOR FILING DATE: 1992-12-07
PRIOR APPLICATION NUMBER: US 08/107,755
PRIOR FILING DATE: 1993-08-19
PRIOR APPLICATION NUMBER: WO 92/14818
PRIOR FILING DATE: 1992-02-12
PRIOR APPLICATION NUMBER: US 07/827,685
PRIOR FILING DATE: 1992-01-30
PRIOR APPLICATION NUMBER: US 07/657,584
PRIOR FILING DATE: 1991-02-19
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 464
TYPE: PRT
ORGANISM: Amsacta moorei entomopoxvirus
US-09-370-861A-2

Query Match 25.8%; Score 48.5; DB 4; Length 464;
Best Local Similarity 57.9%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKF---IDNTLYFI 26

Db 20 INFMMLFFSKIDNNVYPI 38

Search completed: April 23, 2003, 08:19:06
Job time : 31 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:19:14 ; Search time 42 Seconds
(without alignments)
68.683 Million cell updates/sec

Title: US-09-711-896a-1

Perfect score: 188

Sequence: 1 MAAPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB_PEP.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB_PEP.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	100.0	193	9	US-09-770-528-8
2	188	100.0	193	10	US-09-798-075-1
3	176	93.6	193	9	US-10-094-153-3
4	176	93.6	193	9	US-10-094-153-4
5	176	93.6	193	9	US-10-094-153-5
6	176	93.6	193	9	US-10-094-153-9
7	139.5	74.2	133	10	US-09-917-265-2
8	139.5	74.2	192	10	US-09-917-265-8
9	110	58.5	192	9	US-09-770-528-9
10	52	27.7	151	10	US-09-764-864-1231
11	52	27.7	156	10	US-09-864-761-33630
12	52	27.7	445	10	US-09-864-761-46601
13	52	27.7	445	10	US-09-864-761-47605
14	50	26.6	78	9	US-09-749-637A-318
15	49	26.1	285	10	US-09-815-242-4869
16	49	26.1	334	10	US-09-815-242-10798
17	48.5	25.8	264	9	US-09-738-626-5729
18	48.5	25.8	3712	9	US-10-108-605-103
19	47.5	25.3	1806	10	US-09-919-497-56

Sequence 4, Appli
Sequence 39, Appli
Sequence 37, Appli
Sequence 146, Appli
Sequence 2, Appli
Sequence 1447, Ap
Sequence 3369, A
Sequence 32, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 442, App
Sequence 92, Appli
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Sequence 10, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 430, App
Sequence 124, App
Sequence 357, App
Sequence 357, App
Sequence 357, App
Sequence 357, App
Sequence 357, App
Sequence 357, App

US-09-770-528-8
Sequence 8, Application US/09770528
Patent No. US20020164332A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Kastelein, Robert A.
TITLE OF INVENTION: Mammalian Cytokines: Related Reagents
and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:

ALIGNMENTS

RESULT 1

US-09-770-528-8

Sequence 8, Application US/09770528

Patent No. US20020164332A1

GENERAL INFORMATION:

APPLICANT: Hedrick, Joseph A.

Sana, Theodore R.

Kastelein, Robert A.

TITLE OF INVENTION: Mammalian Cytokines: Related Reagents

and Methods

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/770,528

FILING DATE: 25-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/130,972

FILING DATE: <Unknown>

APPLICATION NUMBER: US 60/055,111

FILING DATE: 06-AUG-1997

APPLICATION NUMBER: US 09/062,866

FILING DATE: 20-APR-1998

APPLICATION NUMBER: US 09/097,976

FILING DATE: 16-JUN-1998

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0725K2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-770-528-8

Query Match 100.0%; Score 188; DB 9; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.6e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLESD 36
|||||
1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLESD 36

RESULT 2

US-09-798-075-1
Sequence 1, Application US/09798075
Patent No. US2001004418A1
GENERAL INFORMATION:
APPLICANT: Levy, Shoshana
APPLICANT: Dekryuff, Rosemarie
APPLICANT: Umetsu, Dale
TITLE OF INVENTION: Treatment of Allergies
FILE REFERENCE: STAN-179
CURRENT APPLICATION NUMBER: US/09/798,075
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/188,311
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-075-1

Query Match 100.0%; Score 188; DB 10; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.6e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLESD 36
|||||
1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLESD 36

RESULT 3

US-10-094-153-3
Sequence 3, Application US/10094153
Patent No. US20020169291A1
GENERAL INFORMATION:
APPLICANT: Dinarello, Charles
APPLICANT: Kim, Soo Hyun
TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
FILE REFERENCE: 475
CURRENT APPLICATION NUMBER: US/10/094,153
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/274,327
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 193
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-09-798-075-1

OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-3

Query Match 93.6%; Score 176; DB 9; Length 193;
Best Local Similarity 97.1%; Pred. No. 3.1e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLE 34
|||||
1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENIE 34

RESULT 4

US-10-094-153-4
Sequence 4, Application US/10094153
Patent No. US20020169291A1
GENERAL INFORMATION:
APPLICANT: Dinarello, Charles
APPLICANT: Kim, Soo Hyun
TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
FILE REFERENCE: 475
CURRENT APPLICATION NUMBER: US/10/094,153
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/274,327
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 193
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-4

Query Match 93.6%; Score 176; DB 9; Length 193;
Best Local Similarity 97.1%; Pred. No. 3.1e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLE 34
|||||
1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENIE 34

RESULT 5

US-10-094-153-5
Sequence 5, Application US/10094153
Patent No. US20020169291A1
GENERAL INFORMATION:
APPLICANT: Dinarello, Charles
APPLICANT: Kim, Soo Hyun
TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use
FILE REFERENCE: 475
CURRENT APPLICATION NUMBER: US/10/094,153
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/274,327
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 193
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic PRT Sequence
US-10-094-153-5

Query Match 93.6%; Score 176; DB 9; Length 193;
Best Local Similarity 97.1%; Pred. No. 3.1e-17;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDNTLYFAEDDENLE 34
|||||

Db 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENIE 34

RESULT 6

US-10-094-153-9

; Sequence 9, Application US/10094153

; Patent No. US20020169291A1

; GENERAL INFORMATION:

; APPLICANT: Dinarello, Charles

; APPLICANT: Kim, Soo Hyun

; TITLE OF INVENTION: InterLeukin-18 Mutants, Their Production and use

; FILE REFERENCE: 475

; CURRENT APPLICATION NUMBER: US/10/094,153

; CURRENT FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: 60/274,327

; PRIOR FILING DATE: 2001-03-08

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 193

; TYPE: PRT

; ORGANISM: Artificial Sequence.

; FEATURE:

; OTHER INFORMATION: Synthetic PRT Sequence

US-10-094-153-9

Query Match 93.6%; Score 176; DB 9; Length 193;

Best Local Similarity 97.1%; Pred. No. 3.1e-17;

Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENIE 34

Db 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENIE 34

RESULT 7

US-09-917-265-2

; Sequence 2, Application US/09917265

; Patent No. US20020052030A1

; GENERAL INFORMATION:

; APPLICANT: Wonderling, Ramani S.

; APPLICANT: Boroughs, Karen L.

; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE

; FILE REFERENCE: IM-5

; CURRENT APPLICATION NUMBER: US/09/917,265

; CURRENT FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: 60/223,016

; PRIOR FILING DATE: 2000-08-04

; NUMBER OF SEQ ID NOS: 109

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 133

; TYPE: PRT

; ORGANISM: Felis catus

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (119)..(119)

; OTHER INFORMATION: The 'Xaa' at location 119 stands for Lys, or Asn.

; NAME/KEY: misc.feature

; LOCATION: (470)..(470)

; OTHER INFORMATION: n = unknown at position 470

; OTHER INFORMATION: Xaa = unknown at position 119

US-09-917-265-2

Query Match 74.2%; Score 139.5; DB 10; Length 133;

Best Local Similarity 75.0%; Pred. No. 2.6e-12;

Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENIE 36

Db 1 MTAIPVDD-CINFVGMKFDINTLYFVADSDENLETD 35

RESULT 8

US-09-917-265-8

; Sequence 8, Application US/09917265

; Patent No. US20020052030A1

; GENERAL INFORMATION:

; APPLICANT: Wonderling, Ramani S.

; APPLICANT: Boroughs, Karen L.

; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH

; FILE REFERENCE: IM-5

; CURRENT APPLICATION NUMBER: US/09/917,265

; CURRENT FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: 60/223,016

; PRIOR FILING DATE: 2000-08-04

; NUMBER OF SEQ ID NOS: 109

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Felis catus

US-09-917-265-8

Query Match 74.2%; Score 139.5; DB 10; Length 192;

Best Local Similarity 75.0%; Pred. No. 4e-12;

Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAAEPVEDNCINFVAMKFDINTLYFIAEDDENIE 36

Db 1 MTAIPVDD-CINFVGMKFDINTLYFVADSDENLETD 35

RESULT 9

US-09-770-528-9

; Sequence 9, Application US/09770528

; Patent No. US2002016432A1

; GENERAL INFORMATION:

; APPLICANT: Hedrick, Joseph A.

; Sana, Theodore R.

; Bazan, Fernando J.

; Kastelein, Robert A.

; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents

; and Methods

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/770,528

; FILING DATE: 25-Jan-2001

; CLASSIFICATION: <Unknown>

; PRIORITY INFORMATION:

; APPLICATION NUMBER: 09/130,972

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 60/055,111

; FILING DATE: 06-AUG-1997

; APPLICATION NUMBER: US 09/062,866

; FILING DATE: 20-APR-1998

; APPLICATION NUMBER: US 09/097,976

; FILING DATE: 16-JUN-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0725K2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-852-9196

;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 46601
;; LENGTH: 445
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AF000201.1
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN HELL00, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.8
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
;; OTHER INFORMATION: EST HUMAN HIT: AUI34963.1, EVALUATE 1.00e-130
;; OTHER INFORMATION: SWISSPROT HIT: Q14867, EVALUATE 0.00e+00
US-09-864-761-46601

Query Match 27.7%; Score 52; DB 10; Length 445;
Best Local Similarity 31.8%; Pred. No. 17;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY : 1 MAEPVEDNCINFVAMKFDINT 22
DB 35 LSVHNIEESCFCFLKPKFLDST 56

RESULT 13

US-09-864-761-47605
;; Sequence 47605, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.

;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
;; FILE REFERENCE: Aecmca-x-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 47605
;; LENGTH: 445
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AF124731.2
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.6
;; OTHER INFORMATION: EXPRESSED IN HELL00, SIGNAL = 1
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.74
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
;; OTHER INFORMATION: SWISSPROT HIT: Q14867, EVALUATE 0.00e+00
;; OTHER INFORMATION: EST HUMAN HIT: AUI34963.1, EVALUATE 1.00e-130
US-09-864-761-47605

Query Match 27.7%; Score 52; DB 10; Length 445;
Best Local Similarity 31.8%; Pred. No. 17;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY : 1 MAEPVEDNCINFVAMKFDINT 22
DB 35 LSVHNIEESCFCFLKPKFLDST 56

RESULT 14

US-09-749-637A-318

Sequence 318, Application US/09749637A
Patent No. US2002017349A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cartier, G. Edward
APPLICANT: Watkins, Maren
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert W.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
FILE REFERENCE: 2314-227
CURRENT APPLICATION NUMBER: US/09/749,637A
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/243,412
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US60/219,440
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/173,754
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: PatentIn version 3.0
SEQ ID NO 318
LENGTH: 78
TYPE: PRT
ORGANISM: Conus imperialis
US-09-749-637A-318

Query Match 26.6%; Score 50; DB 9; Length 78;
Best Local Similarity 34.8%; Pred. No. 4.7;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 10 CINFVAMKFIDNTLYFIAEDDEN 32
I: |||: |:: |:
DB 5 CVFVAVPFLTASVFITADSRN 27

RESULT 15
US-09-815-242-4869
Sequence 4869, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4869
LENGTH: 285
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-815-242-4869
Query Match 26.1%; Score 49; DB 10; Length 285;
Best Local Similarity 33.3%; Pred. No. 28;
Matches 10; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
QY 6 VEDNCINFVAMKFIDNTLYFIAEDDEN 35
I: |||: |:: |:
DB 69 IQDMLVELENTNFIDTILFLDADDEELVS 98
Search completed: April 23, 2003, 08:25:16
Job time : 43 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 23, 2003, 08:16:39 ; Search time 43 seconds
(without alignments)
80.485 Million cell updates/sec

Title: us-09-711-896A-1

Perfect score: 186

Sequence: 1 MAAPVEDNCINFVAMKFDNTLYFIAEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	58.5	192	2 S60226	cytokine IGIF - mouse
2	62.5	33.2	1398	2 H71606	hypothetical prote
3	56	29.8	780	2 T29700	hypothetical prote
4	55	28.3	275	2 G89961	hypothetical prote
5	55	29.3	687	2 S53485	carnitine O-acetyl
6	53	28.2	365	2 E81307	succinyl-diaminopi
7	52.5	27.9	212	2 G97866	hypothetical prote
8	52	27.7	736	2 T00023	transcription fact
9	51	27.1	647	2 T28214	probable nucleosid
10	50	26.6	302	2 T38789	hypothetical prote
11	50	26.6	536	2 A36590	ecdysteroid recept
12	50	26.6	908	2 A82254	hypothetical prote
13	49.5	26.3	1009	2 T16604	hypothetical prote
14	49	26.1	327	2 E97088	beta-xylosidase, f
15	49	26.1	338	2 A82890	hypothetical prote
16	49	26.1	490	2 H96911	uroporphyrinogen I
17	49	26.1	747	1 VPAR45	outer layer protei
18	49	26.1	776	1 VPXR31	outer layer protei
19	49	26.1	776	1 VPXR31	outer layer protei
20	49	26.1	776	2 S24410	hypothetical outer
21	49	26.1	1628	2 T38055	hypothetical prote
22	48.5	25.8	285	2 T09308	immediate-early pr
23	48.5	25.8	299	2 JC4374	sterol uptake prot
24	48.5	25.8	384	2 F81354	DNA /pantothenate
25	48.5	25.8	464	1 WZVZG1	GIL protein - Amsa
26	48.5	25.8	1218	2 T1376	glutamate receptor
27	48.5	25.8	3712	2 S18253	laminin alpha-1 ch
28	48	25.5	209	2 H90128	hypothetical prote
29	48	25.5	480	2 T34102	hypothetical prote

30	47.5	25.3	284	2 A83688	hypothetical prote
31	47.5	25.3	367	2 T19937	hypothetical prote
32	47.5	25.3	482	2 B31795	collagen alpha 1(X
33	47.5	25.3	532	2 T02539	hypothetical prote
34	47.5	25.3	673	2 T15551	hypothetical prote
35	47.5	25.3	888	2 S28791	collagen alpha 1(X
36	47.5	25.3	1435	2 S54697	DNA polymerase III
37	47.5	25.3	1435	2 C90596	hypothetical prote
38	47.5	25.3	1806	1 CGHUIE	collagen alpha 1(X
39	47	25.0	250	2 S69031	hypothetical prote
40	47	25.0	316	2 S75062	transcription regu
41	47	25.0	357	2 T38405	hypothetical prote
42	47	25.0	443	1 AJCLOA	glutamate-ammonia
43	47	25.0	468	2 B72351	clostripain-relate
44	47	25.0	502	2 T29729	hypothetical prote
45	47	25.0	571	2 S58356	pept protein - Sta

ALIGNMENTS

RESULT 1

S60226

cytokine IGIF - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000

C:Accession: S60226

R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig

Nature 378, 88-91, 1995

A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.

A:Reference number: S60226; MUID:96061009; PMID:7477296

A:Accession: S60226

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OK>

A:Cross-references: EMBL:D49949; NID:gl064822; PIDN:BAA08705.1; PID:gl064823

C:Superfamily: Mus musculus cytokine IGIF

Query Match

Best Local Similarity 58.5%; Score 110; DB 2; Length 192;

Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINFVAMKFDNTLYFIAEDDENLESD 36

Db 6 EDCVNFKEMFIDNTLYFIPEENGLESD 35

RESULT 2

H71606

hypothetical protein PFB0755w - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000

C:Accession: H71606

R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E

.; Perle, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H

Science 282, 1126-1132, 1998

A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A:Reference number: A71600; MUID:99021743; PMID:9804551

A:Accession: H71606

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1398 <GAR>

A:Cross-references: GB:AE001416; NID:g3845268; PIDN:AAC71940.1; PID:g384

A:Experimental source: clone 3D7

C:Genetics:

A:Gene: PFB0755w

Query Match

Best Local Similarity 33.2%; Score 62.5; DB 2; Length 1398;

Matches 13; Conservative 8; Mismatches 11; Indels 9; Gaps 1;

QY 4 EPVEDNCINFVAMKFI-----DNTLYFIAEDDENLESD 35

A:Reference number: A97700; MUID:21442074; PMID:11557893
 A:Accession: G97866
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-212 <KUR>
 A:Cross-references: GB:AE006914; PIDN:AAL03873.1; PID:gl5620478; GSPDB:GN00173
 C:Genetics:
 A:Gene: RC1335

Query Match 27.9%; Score 52.5; DB 2; Length 212;
 Best Local Similarity 36.1%; Pred. No. 9.1;
 Matches 13; Conservative 5; Mismatches 7; Indels 11; Gaps 1;
 QY 12 NFVAMKFD-----NTLYFTAEDDENLESD 36
 ||||| I || I: || I: I
 Db 84 NFVSMYDYDMEQVSRINRSNTFNFLEEDNEHLDDK 119

RESULT 8
 T00023
 Transcription factor BACH1 [imported] - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 28-Jul-2000
 C:Accession: T00023; T08879
 R:Ohira, M.; Seki, N.; Nagase, T.; Ishikawa, K.; Nomura, N.; Ohara, O.
 Genomics 47, 300-306, 1998
 A:Title: Characterization of a human homolog (BACH1) of the mouse Bach1 gene encoding a
 A:Reference number: Z14060; MUID:98140130; PMID:9479503
 A:Accession: T00023
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-736 <OHI>
 A:Cross-references: EMBL:AB002803; PIDN:BAA24932.1
 A:Experimental source: immature myeloid
 R:Blouin, J.L.; Duriaux Sail, G.; Guipponi, M.; Rossier, C.; Pappasavas, M.P.; Antonarak
 Hum. Genet. 102, 282-288, 1998
 A:Title: Isolation of the human BACH1 transcription regulator gene, which maps to chromo
 A:Reference number: Z16510; MUID:98204399; PMID:9544839
 A:Accession: T08879
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-157, T', 159-170, 'G', 172-736 <BLO>
 A:Cross-references: EMBL:AF026199; MUID:92565399; PID:92565400
 C:Genetics:
 A:Gene: BACH1
 A:Map position: 21q22.1
 C:Superfamily: human transcription factor BACH1; POZ domain homology
 C:Keywords: leucine zipper; transcription factor; transcription regulation; zinc finger
 F:20-122/Domain: POZ domain homology <POZ>

Query Match 27.7%; Score 52; DB 2; Length 736;
 Best Local Similarity 31.8%; Pred. No. 39;
 Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MAEPVEDNCINFAVKFDINT 22
 :: :||: I: ||: I
 Db 113 LSVHNIEESCFQFKFKFLDST 134

RESULT 9
 T28214
 Probable nucleoside-triphosphatase (EC 3.6.1.15) - Melanoplus sanguinipes entomopoxvirus
 N:Alternate names: putative nucleoside triphosphate phosphohydrolase
 C:Species: Melanoplus sanguinipes entomopoxvirus
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 17-Nov-2000
 C:Accession: T28214
 R:Afonso, C.D.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
 J. Virol. 73, 533-552, 1999
 A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
 A:Reference number: Z20484; MUID:99102612; PMID:9847359
 A:Accession: T28214
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-647 <AFO>
 A:Cross-references: EMBL:AF063866; MUID:g4049647; PIDN:AAC97824.1; PID:g4049864
 A:Experimental source: isolate Tuscon
 C:Genetics:
 A:Note: MSV053
 C:Superfamily: vaccinia virus nucleoside-triphosphatase I
 C:Keywords: ATP; hydrolase; P-loop

Query Match 27.1%; Score 51; DB 2; Length 647;
 Best Local Similarity 31.1%; Pred. No. 47;
 Matches 14; Conservative 7; Mismatches 10; Indels 14; Gaps 1;
 QY 3 AEPVEDNCI-----NFVAMKFDINTLYFTAEDDENL 33
 ||||| I || I: || I: I
 Db 554 AEPVENEIFNIRTKIDDVNNENNVITKIIVSYCSDELNI 598

RESULT 10
 T38789
 Hypothetical protein SPAC4C5.03 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38789
 R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream Wood, V.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21811
 A:Accession: T38789
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-302 <PEA>
 A:Cross-references: EMBL:Z98560; PIDN:CAB11174.1; GSPDB:GN000066; SPDB:SPAC4C5.03
 A:Experimental source: strain 972h-; cosmid c4C5
 C:Genetics:
 A:Gene: SPDB:SPAC4C5.03
 A:Map position: 1

Query Match 26.6%; Score 50; DB 2; Length 302;
 Best Local Similarity 34.8%; Pred. No. 29;
 Matches 8; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 10 CINFVAMKFDINTLYFTAEDDEN 32
 I: :||: I: ||||
 Db 115 CVLMAFMFLPRPIHFVAADEN 137

RESULT 11
 A56590
 ecdysteroid receptor homolog cEcRH - midge (Chironomus tentans)
 C:Species: Chironomus tentans
 C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Sep-1999
 C:Accession: A56590
 R:Imhof, M.O.; Rusconi, S.; Lezzi, M.
 Insect Biochem. Mol. Biol. 23, 115-124, 1993
 A:Title: Cloning of a Chironomus tentans cDNA encoding a protein (cEcRH) homologous
 A:Reference number: A56590; MUID:93250857; PMID:8485513
 A:Accession: A56590
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-536 <IMH>
 A:Cross-references: GB:S60739; MUID:9385893; PIDN:AAC60500.1; PID:g385894
 A:Note: sequence extracted from NCBI backbone (NCBIN:132124, NCBIP:132127)
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: DNA binding; steroid hormone receptor; zinc finger
 F:113-432/Domain: erba transforming protein homology <ERBA>

Query Match 26.6%; Score 50; DB 2; Length 536;
 Best Local Similarity 38.5%; Pred. No. 53;
 Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 11 INFVAMKFDINTLYFTAEDDENLESD 36
 :||: ||: ||: ||||
 Db 16 LNYASOSFGDNNIYGATKKQRLSD 41

```

A:Molecule type: DNA
A:Residues: 1-327 <KUR>
A:A/Cross-references: GB:AE001437; PIDN:AAK79496.1; PID:q15024478; GSPDB:GN00168
A:A/Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
C:Gene: CAG1529
C:Superfamily: Streptomyces chartreusis alpha-L-arabinofuranosidase II

Query Match 26.1%; Score 49; DB 2; Length 327;
Best Local Similarity 32.6%; Pred. No. 44;
Matches 15; Conservative 6; Mismatches 13; Indels 12; Gaps 2;

QY 3 AEPVE-----DNCINFAVKFIDNT--LYFIAEDDENLESD 36
||||| : : : : : : : : : : : : : : : : : :
DB 53 AEPVDVRRHSGMSNLINWAPETHFINGAWIYFAAAPDKNIEDD 98

RESULT 15
A82890
C:Species: Ureaplasma urealyticum
C:date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82890
R:Glass, J.I.; Leftkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to Genbank, February 2000

```

C;date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82890
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
A;Reference number: A82870
A;Accession: A82890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-338 <GLA>
A;Cross-references: GB:AE002141; GB:AF222894; NID:56899434; PIDN:AAF30863.1; GSPDB:G
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU451
A;Genetic code: SGC3

Qy 3 APEVEDCINFAVMKFDINTLYIAEDDENSEL 36
| : | : | : | : | : | : | : | : |
Db 225 AOLVDECLLAPOSSEVFENNEYFEEVEYHDPD 258

Search completed: April 23, 2003, 08:20:39
Job time : 46 secs

1. *Chlorophyll a* and *Chlorophyll b* were determined using a spectrophotometer (Shimadzu UV-160U) at 663 nm and 646 nm, respectively. The concentration of chlorophyll was calculated using the following formula: $\text{Chlorophyll concentration (mg/L)} = \frac{\text{Absorbance} \times 1000}{\text{Path length (cm)}} \times \text{Extinction coefficient}$.

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

2. Next, it is important to gather relevant information and data. This can be done through research, consultation with experts, or by analyzing existing data sets.

3. Once the information is gathered, the next step is to analyze it. This involves identifying patterns, trends, and potential solutions. It is important to consider all relevant factors and to evaluate the feasibility of different options.

4. After analysis, the next step is to develop a plan or strategy. This involves determining the most effective way to address the problem or question, taking into account the available resources and the potential risks.

5. The final step is to implement the plan and monitor the results. This involves putting the plan into action and tracking progress to ensure that the problem is being addressed effectively. If necessary, adjustments should be made to the plan based on the results.

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:16:39 ; Search time 11 seconds
(without alignments)
135.741 Million cell updates/sec

Title: US-09-711-896a-1

Perfect score: 188

Sequence: 1 MAAPVEDNCINFVAMKFDNTLYFAEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	188	100.0	193	1	1	IL18_HUMAN	Q14116 homo sapien
2	159	84.6	193	1	1	IL18_HORSE	Q9xsq7 equus caball
3	147.5	78.5	192	1	1	IL18_PIG	Q19073 sus scrofa
4	146	77.7	193	1	1	IL18_BOVIN	Q9tu73 bos taurus
5	136	72.3	193	1	1	IL18_CANFA	Q9xsr0 canis famil
6	110	58.5	192	1	1	IL18_MOUSE	P70380 mus musculus
7	109	58.0	194	1	1	IL18_RAT	P97636 rattus norv
8	55	29.3	688	1	1	CACM_YEAST	P80235 saccharomyc
9	52.5	27.9	183	1	1	LGUL_MOUSE	Q9cpu0 mus musculus
10	52	27.7	736	1	1	BAC1_HUMAN	Q14867 homo sapien
11	52	27.7	739	1	1	BAC1_MOUSE	P97302 mus musculus
12	51	27.1	647	1	1	NTP1_MSEPV	Q9yw39 melanoplus
13	50	26.6	302	1	1	YDX3_SCHPO	Q14166 schizosacch
14	50	26.6	536	1	1	ECR_CHITE	P49882 chironomus
15	49	26.1	776	1	1	VP41_ROTST	P04508 smian l1 r
16	49	26.1	776	1	1	VP4_ROTBC	P08713 bovine rota
17	49	26.1	776	1	1	VP4_ROTSP	P17463 simian l1 r
18	49	26.1	1628	1	1	YABE_SCHPO	Q09779 schizosacch
19	48.5	25.8	299	1	1	SUT1_YEAST	P53032 saccharomyc
20	48.5	25.8	464	1	1	VGIL_AMEPV	P29817 ansacta moo
21	48.5	25.8	855	1	1	GCFC_MOUSE	P58501 mus musculus
22	48.5	25.8	3712	1	1	LMA_DROME	Q00174 drosophila
23	47.5	25.3	482	1	1	CA1B_RAT	P20909 rattus norv
24	47.5	25.3	1435	1	1	DPO3_MYCPU	P47729 mycoplasma
25	47.5	25.3	1806	1	1	CA1B_HUMAN	P12107 homo sapien
26	47	25.0	357	1	1	YFQB_SCHPO	Q10170 schizosacch
27	47	25.0	443	1	1	GLNA_CLOSA	P10656 clostridium
28	47	25.0	690	1	1	ATM1_YEAST	P40416 saccharomyc
29	47	25.0	774	1	1	VP4_ROTHT	P11200 human rotav
30	47	25.0	775	1	1	VP4_ROTHT	P11197 human rotav
31	47	25.0	776	1	1	VP4_ROTHT	P36305 bovine rota
32	47	25.0	776	1	1	VP4_ROTHT	P11199 human rotav
33	47	25.0	2146	1	1	INSR_DROME	P09208 drosophila

RESULT 1

IL18_HUMAN
ID IL18_HUMAN STANDARD: PRT: 193 AA.
AC Q14116; 075599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
in Escherichia coli, and studies on the biologic activities of the
protein.";
RT J. Immunol. 156:4274-4279(1996).
RL [2]
RN SEQUENCE FROM N.A.
RA Yong D., Guixin D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RL [3]
RN SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human interleukin 18 cDNA.";
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL [4]
RN SEQUENCE FROM N.A.
RA Strausberg R.;
RT TISSUE=Urinary bladder;
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RL [5]
RN SEQUENCE OF 2-193 FROM N.A.
RC TISSUE=Peripheral blood;
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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DR EMBL; D49950; BAA08706.1;
 DR EMBL; AF077611; AAC27787.1;
 DR EMBL; AY044641; AAK95950.1;
 DR EMBL; BC007007; AAH07007.1;
 DR EMBL; BC007461; AAH07461.1;
 DR EMBL; U90434; AAB50010.1;
 DR Genew; HGNC:5986; IL18.
 DR MIN; 600953;
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 36
 FT CHAIN 37 193
 FT CONFLICT 66 66
 FT CONFLICT 86 86
 FT CONFLICT 191 191
 FT SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;
 BY SIMILARITY.
 INTERLEUKIN-18.
 F -> L (IN REF. 2).
 S -> R (IN REF. 2).
 N -> S (IN REF. 2).

Query Match 100.0%; Score 188; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 9.3e-20;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36
 |||||
 DB 1 MAAPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36

RESULT 2
 IL18_HORSE
 ID IL18_HORSE STANDARD; PRT; 193 AA.
 AC QX507;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma)
 DE IL18 OR IGIF.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 NColson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
 Argyle D.J., Onions D.E.,
 "Nucleotide sequence of equine interleukin 12 and 18 cDNAs."
 Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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DR EMBL; Y11131; CAA72013.1;
 KW Cytokine.
 FT PROPEP 1 36
 FT CHAIN 37 193
 FT SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAF CRC64;
 BY SIMILARITY.
 INTERLEUKIN-18.

Query Match 84.6%; Score 159; DB 1; Length 193;
 Best Local Similarity 83.3%; Pred. No. 1.3e-15;
 Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36
 |||||
 DB 1 MAAPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36

RESULT 3
 IL18_PIG
 ID IL18_PIG STANDARD; PRT; 192 AA.
 AC O19073;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 37, Last sequence update)
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma)
 DE IL18 OR IGIF.
 GN Sus scrofa (Pig).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Foss D.L., Murtough M.P.;
 RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muneta Y., Mori Y.;
 RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=20260994; PubMed=10803849;
 RA Fournout S., Dozois C.M., Verle M., Pinton P., Fairbrother J.M.,
 RA Oswald E., Oswald I.P.;
 RT "Cloning, chromosomal location, and tissue expression of the gene for
 RT pig interleukin-18."
 RT Immunogenetics 51:358-365(2000).

CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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DR EMBL; U68701; AAC18415.1;
 DR EMBL; AB010003; BAA24135.1;
 DR EMBL; AF191088; AAF71200.1;
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35
 FT CHAIN 36 192
 FT SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;
 BY SIMILARITY.
 INTERLEUKIN-18.

Query Match 78.5%; Score 147.5; DB 1; Length 192;
 Best Local Similarity 80.6%; Pred. No. 5.8e-14;
 Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36
 |||||
 DB 1 MAAPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 35

RESULT 4
 IL18_BOVIN
 ID IL18_BOVIN STANDARD; PRT; 193 AA.

DR MGD; MGI:107936; IL18.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35
 FT CHAIN 36 192 INTERLEUKIN-18.
 FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
 SQ SEQUENCE 192 AA; 8PD938473874D63 CRC64;
 Query Match 58.5%; Score 110; DB 1; Length 192;
 Best Local Similarity 66.7%; Pred. No. 1.3e-08;
 Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 7 EDNCINFAVKFIDNTLYFAEDDENLSD 36
 DB 6 EDCVNFKEKMFIDNTLYFPEENGLED 35
 ID IL18_RAT STANDARD; PRT; 194 AA.
 AC P97636; P97637; O88749;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
 GN IL18 OR IGIF.
 OS Rattus norvegicus (Rat)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
 RX MEDLINE=97152963; PubMed=8998986;
 RA Conti B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
 RA "Induction of Interferon-gamma inducing factor in the adrenal
 cortex.";
 RT J. Biol. Chem. 272:2035-2037(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=98368130; PubMed=9702748;
 RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
 RA "Cloning of rat brain interleukin-18 cDNA.";
 RT Mol. Psych. 3:362-366(1998).
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CC CELLS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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 CC EMBL; U77776; AAC53009.1;
 DR EMBL; U77777; AAC53010.1;
 DR EMBL; AJ222813; CAAL1001.1;
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR SMART; SM00125; IL1; 1.
 KW Cytokine; Alternative splicing.
 FT PROPEP 1 36
 FT CHAIN 37 194 INTERLEUKIN-18.
 FT VARSPLIC 121 139 MISSING (IN ISOFORM ALPHA).
 FT CONFLICT 4 5 MS -> IP (IN REF. 2).
 FT

FT CONFLICT 48 48 I1 -> M (IN REF. 2).
 SQ SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;
 Query Match 58.0%; Score 109; DB 1; Length 194;
 Best Local Similarity 61.1%; Pred. No. 1.9e-08;
 Matches 22; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFAVKFIDNTLYFAEDDENLSD 36
 DB 1 MAAMSEGCNVNFKEKMFIDNTLYLIPEDNGDLED 36
 ID CACM_YEAST STANDARD; PRT; 688 AA.
 AC P80235;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Putative mitochondrial carnitine O-acetyltransferase (EC 2.3.1.7).
 GN YAT1 OR YAR035W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DL-1;
 RX MEDLINE=94086564; PubMed=8262985;
 RA Schmalix W., Bandlow W.
 RT "The ethanol-inducible YAT1 gene from yeast encodes a presumptive
 RT mitochondrial outer carnitine acetyltransferase.";
 RL J. Biol. Chem. 268:27428-27439(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C; AB972;
 RX MEDLINE=95249563; PubMed=7731988;
 RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
 RA Hall J., Ouellette B.F., Keng T., Barton A.B., Su Y., Davies C.K.,
 RA Storms R.K.;
 RA "The nucleotide sequence of chromosome I from Saccharomyces
 RA cerevisiae";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
 CC -1- FUNCTION: INVOLVED IN THE TRANSFER OF ACETYL-COA INTO
 CC MITOCHONDRIA. MAY ALSO BE INVOLVED IN THE METABOLISM OF ACETATE
 CC AND OF ETHANOL.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + carnitine = CoA + O-
 CC acetylcarnitine
 CC -1- PATHWAY: SECOND STEP IN TRANSPORT OF FATTY ACIDS INTO
 CC MITOCHONDRIA.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane; outer side.
 CC -1- INDUCTION: BY ETHANOL AND BY ACETATE. REPRESSED BY GLUCOSE,
 CC AND TO A LESSER EXTENT, BY GALACTOSE. DEREPRESSED BY GLYCEROL.
 CC -1- SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACETYLTRANSFERASE
 CC FAMILY.
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 CC EMBL; X74553; CAAS2647.1;
 DR EMBL; L28920; AAC09495.1;
 DR PIR; S36631; S36631.
 DR PIR; S47902; S47902.
 DR SGD; S0000080; YAT1;
 DR InterPro; IPR000542; Carn_acyltransf.
 DR Pfam; PF00755; Carn_acyltransf; 1.
 DR PROSITE; PS00439; ACYLTRANSF_C1; FALSE_NEG.
 DR PROSITE; PS00440; ACYLTRANSF_C2; 1.

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CC EMBL; AK002386; BAB22060.1; -
CC EMBL; AK003567; BAB22863.1; -
CC EMBL; AK005055; BAB23781.1; -
CC HSP; Q04760; IQIP.
CC MGD; MGI:95742; Glol.
CC InterPro; IPR004361; Glyoxalase_1.
CC InterPro; IPR004360; Gly_bleo_diox.
CC Pfam; PF00903; Glyoxalase; 1.
CC ProDom; PD002334; Glyoxalase_1; 1.
CC TIGRfams; TIGR00068; glyox_I; 1.
CC PROSITE; PS00934; GLYOXALASE_I_1; 1.
CC PROSITE; PS00935; GLYOXALASE_I_2; 1.
CC Lyase; Zinc.
CC INIT_MET 0 0 BY SIMILARITY.
CC METAL 33 33 ZINC (BY SIMILARITY).
CC METAL 99 99 ZINC (BY SIMILARITY).
CC METAL 126 126 ZINC (BY SIMILARITY).
CC METAL 172 172 ZINC (BY SIMILARITY).
CC SEQUENCE 183 AA; 20678 MW; 8B9EF0A1D845002C CRC64;
Query Match 27.9%; Score 52.5; DB 1; Length 183;
Best Local Similarity 50.0%; Pred.No.2.1;
Matches 11; Conservative 6; Mismatches 2; Indels 3; Gaps 1;
QY 11 INFVAMKFDNTLYFTAEDDEN 32
DB 60 LDPFAMKFS---SLYFLAYEDKN 78
:::|||||::|::|::|::|::|::|
RESULT 10
BAC1_HUMAN STANDARD; PRT; 736 AA.
ID BAC1_HUMAN
AC 014867; 043285;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription regulator protein BACH1 (BTB and CNC homolog 1)
DE (HA2303).
DE GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98204399; PubMed=9544839;
RX Blouin J.-L., Durlaux Sall G., Guipponi M., Rossier C.,
RX Pappasavas M.-P., Antonarakis S.E.;
RX "Isolation of the human BACH1 transcription regulator gene, which
RX maps to chromosome 21q22.1.";
RX Hum. Genet. 102:282-288(1998).
RX [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=98140130; PubMed=9479503;
RX Chira M., Seki N., Nagase T., Ishikawa K., Nomura N., Ohara O.;
RX "Characterization of a human homolog (BACH1) of the mouse Bach1 gene
RX encoding a BTB-basic leucine zipper transcription factor and its
RX mapping to chromosome 21q22.1.";
RX Genomics 47:300-306(1998).
RX [3]
RX SEQUENCE FROM N.A.
RX Taudien S., Dagand E., Delabar J., Nordsiek G., Drescher B., Weber J.,
RX Schattevoy R., Yaspo M.-L., Rosenthal A.;
RX Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RX [4]
RX SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RX Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RX Park H.-S., Toyoda A., Ishii K., Toki Y., Choi D.-K., Soeda E.,
RX Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,

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RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Reintshal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordisiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ranser J., Beck A., Klages S., Hennig S., Blessemann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.,
RT Nature 405:311-319(2000).
RL
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS AS REPRESSOR OR
CC ACTIVATOR. BINDS, IN-VITRO, TO NF-E2 BINDING SITES. PLAY IMPORTANT
CC ROLES IN COORDINATING TRANSCRIPTION ACTIVATION AND REPRESSION BY
CC MAFK.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE BZIP FAMILY. CNC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC
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CC
DR EMBL; AF026199; AAB84100.1; -
DR EMBL; AF026200; AAB84101.1; -
DR EMBL; AF026203; BAA24932.1; -
DR EMBL; AF124731; AAD14689.1; -
DR EMBL; AL163249; CAB90435.1; -
DR EMBL; AP001705; BAA95505.1; -
DR HSSP; P34707; ISKN.
DR TRANSFAC; T04791; -
DR TRANSFAC; T04798; -
DR GENIE; HGNC:935; BACH1.
DR MIM; 602751; -
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR004827; TF_BZIP.
DR Pfam; PF00170; BZIP; 1.
DR Pfam; PF00651; BTB; 1.
DR SMART; SM00338; BRLZ; 1.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS00036; BZIP_BASIC; 1.
DR
KW Transcription regulation; Activator; Repressor; DNA-binding;
Nuclear protein.
FT DOMAIN 34 100 BTB.
FT DNA_BIND 562 577 BASIC MOTIF.
FT DOMAIN 585 607 LEUCINE-ZIPPER.
FT CONFLICT 158 158 S -> T (IN REF. 1).
FT CONFLICT 171 171 E -> G (IN REF. 1).
SQ SEQUENCE 736 AA; 81957 MW; CAAEECC63D46571B CRC64;

Query Match 27.7%; Score 52; DB 1; Length 736;
Best Local Similarity 31.8%; Pred. No. 12;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDINT 22
Db 113 LSVHNIESCQFLKFKFLDST 134

RESULT 11
BACH1_MOUSE
AC p97302; STANDARD; PRT; 739 AA.
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription regulator protein BACH1 (BTB and CNC homolog 1).
GN BACH1.

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OS Mus musculus; (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX MEDLINE=97042438; PubMed=8887638;
RA Oyake T., Itoh K., Motoshashi H., Hayashi N., Hoshino H., Nishizawa M.,
RA Yamamoto M., Igarashi K.;
RT "Bach proteins belong to a novel family of BTB-basic leucine zipper
RT transcription factors that interact with MafK and regulate
RT transcription through the NF-E2 site.";
RL Mol. Cell. Biol. 16:6083-6095(1996).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS AS REPRESSOR OR
CC ACTIVATOR. BINDS, IN-VITRO, TO NF-E2 BINDING SITES. PLAY IMPORTANT
CC ROLES IN COORDINATING TRANSCRIPTION ACTIVATION AND REPRESSION BY
CC MAFK.
CC -!- SUBUNIT: HETERODIMER OF BACH1 AND MAFK.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: UBIQUITOUS.
CC -!- SIMILARITY: BELONGS TO THE BZIP FAMILY. CNC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC
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CC
DR EMBL; D86603; BAA13137.1; -
DR HSSP; P34707; ISKN.
DR TRANSFAC; T04793; -
DR MGD; MGI:894680; Bach1.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR004827; TF_BZIP.
DR Pfam; PF00170; BZIP; 1.
DR Pfam; PF00651; BTB; 1.
DR SMART; SM00338; BRLZ; 1.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS00036; BZIP_BASIC; 1.
DR
KW Transcription regulation; Activator; Repressor; DNA-binding;
Nuclear protein.
FT DOMAIN 34 100 BTB.
FT DNA_BIND 562 580 BASIC MOTIF.
FT DOMAIN 588 610 LEUCINE-ZIPPER.
SQ SEQUENCE 739 AA; 81373 MW; CE2DE606B05F6B32 CRC64;

Query Match 27.7%; Score 52; DB 1; Length 739;
Best Local Similarity 31.8%; Pred. No. 12;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAEPVEDNCINFVAMKFDINT 22
Db 113 LSVHNIESCQFLKFKFLDST 134

RESULT 12
NTP1_MSEPV
ID 1 NTP1_MSEPV STANDARD; PRT; 647 AA.
AC Q9Y39;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nucleoside triphosphatase I (EC 3.6.1.15) (Nucleoside triphosphate
DE phosphohydrolase I) (NPH I).
DE MSV053.
GN Melanoplus sanguinipes entomopoxvirus (MsePV).
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.

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Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Mottier S.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gallardin C., Tallada V.A., Carlson A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutini L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe";
Nature 415:871-880(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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EMBL; Z98560; CAB1174.1;
Hypothetical protein; Transmembrane.
TRANSMEM 25 45 POTENTIAL.
TRANSMEM 58 78 POTENTIAL.
TRANSMEM 104 124 POTENTIAL.
TRANSMEM 158 178 POTENTIAL.
TRANSMEM 182 202 POTENTIAL.
TRANSMEM 215 235 POTENTIAL.
TRANSMEM 247 267 POTENTIAL.
SEQUENCE 302 AA; 33854 MW; OD7D7AB3D21E3C12_CRC64;
Query Match 26.6%; Score 50; DB 1; Length 302;
Best Local Similarity 34.8%; Pred. No. 8.6;
Matches 8; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
Oy 10 CINFVAMKFDINTLYPIAEDDEN 32
db 115 CVMIAFWFMFLPRPIHFVAADEN 137

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RESULT 14	ECR_CHITE	STANDARD;	PRT;	536 AA
AC	ECR_CHITE			
AC	P49882;			
DT	01-OCT-1996	(Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	Ecdysone receptor (Ecdysteroid receptor)	(20E-hydroxy-ecdysone receptor) (ECRH).		
DE	ECR OR NR1H1			
OS	Chironomus tentans (Midge)			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata;	Pancrustacea; Hexapoda;		
OC	Insecta; Pterygota; Neoptera; Endopterygota;	Diptera; Nematocera;		
OC	Chironomidae; Chironomidae; Chironominae;	Chironomus.		
OX	NCBI_TaxID=7153;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RRX	MEDLINE=93250857; PubMed=8485513;			
RA	Imhof M.O., Rusconi S., Lezzi M.;			
RT	"Cloning of a Chironomus tentans cDNA encoding a protein (cECRH)			
RT	homologous to the Drosophila melanogaster ecdysteroid receptor			
RT	(dECR)."			
RRL	Insect Biochem. Mol. Biol. 23:115-124 (1993).			
CC	!- FUNCTION: RECEPTOR FOR ECDYSONE. BINDS TO ECDYSONE RESPONSE			
CC	ELEMENTS (ECRES).			
CC	!- SUBCELLULAR LOCATION: Nuclear.			

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OM protein - protein search, using sw model

Run on: April 23, 2003, 08:16:39 ; Search time 84 Seconds
(without alignments)
88.306 Million cell updates/sec

Title: US-09-711-896A-1

Perfect score: 188

Sequence: 1 MAAEPEVDNCINFAVKFIDNTLYFAEDDENLESD 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*

- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp-invertebrate.*
- 6: sp-mammal.*
- 7: sp-mhc.*
- 8: sp-organelle.*
- 9: sp-phage.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp-unclassified.*
- 15: sp-rvivirus.*
- 16: sp-bacteriap.*
- 17: sp-archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	188	100.0	193	4	Q96KJ8
2	179	95.2	193	6	Q9BG15
3	155	82.4	193	6	Q9GL09
4	147.5	78.5	192	6	Q9NLP7
5	143.5	76.3	192	6	Q9SM33
6	110	58.5	196	11	Q91266
7	93	49.5	178	6	Q9MZL8
8	62.5	33.2	1398	5	Q9G244
9	55	29.3	275	16	Q99TA3
10	54	28.7	417	5	Q9G410
11	53.5	28.5	1055	12	Q65146
12	53	28.2	70	2	Q9JN03
13	53	28.2	365	16	Q9PNP3
14	53	28.2	1039	5	Q9GV97
15	52.5	27.9	149	11	Q9DB53
16	52.5	27.9	184	11	Q9R3T1

17	52.5	27.9	212	16	Q92F22	Q92fz2 rickettsia
18	51.5	27.4	186	10	Q93YC4	Q93yc4 nicotiana t
19	51.5	27.4	384	10	Q93YE7	Q93ye7 nicotiana t
20	51.5	27.4	425	10	Q9XG72	Q9xg72 nicotiana t
21	51.5	27.4	425	10	Q93YD6	Q93yd6 nicotiana t
22	51.5	27.4	425	10	Q93YB9	Q93yb9 nicotiana t
23	51.5	27.4	426	10	Q93YE0	Q93ye0 nicotiana t
24	51	27.1	608	2	Q93A37	Q93a37 acinetobact
25	50.5	26.9	202	12	Q9DWF2	Q9dfw2 rat cytomeg
26	50.5	26.9	202	13	Q8QH55	Q8qh55 malurus mel
27	50.5	26.9	308	16	Q8RGK4	Q8rgk4 fusobacteri
28	50.5	26.9	384	10	Q93YF0	Q93yf0 nicotiana t
29	50	26.6	326	16	Q8XN37	Q8xn37 clostridium
30	50	26.6	908	16	Q8YR62	Q8yr62 anabaena sp
31	49.5	26.3	547	4	Q9HAY6	Q9hay6 homo sapien
32	49.5	26.3	547	4	Q9NVH5	Q9nvh5 homo sapien
33	49.5	26.3	722	12	Q8QLN0	Q8qln0 mamestra co
34	49.5	26.3	954	12	Q9IN15	Q9in15 banna virus
35	49.5	26.3	1009	5	Q99994	Q99994 caenorhabdi
36	49	26.1	308	2	Q9X5Y9	Q9x5y9 thriobacillu
37	49	26.1	327	16	Q97IW1	Q97iw1 clostridium
38	49	26.1	338	16	Q9PQ39	Q9pq39 ureaplasma
39	49	26.1	376	2	Q8VTZ0	Q8vtz0 leptospira
40	49	26.1	376	2	Q8VTW0	Q8vtw0 leptospira
41	49	26.1	376	2	Q8VLF1	Q8vlf1 leptospira
42	49	26.1	490	16	Q97M03	Q97mu3 clostridium
43	49	26.1	552	5	O45117	O45117 chironomus
44	49	26.1	588	10	Q9FLM7	Q9flm7 arabidopsis
45	49	26.1	776	12	Q96802	Q96802 rotavirus a

ALIGNMENTS

RESULT 1

Q96KJ8 PRELIMINARY; PRT; 193 AA;
AC Q96KJ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF380360; AAK57024.1;
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 100.0%; Score 188; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 7.2e-19;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAEPEVDNCINFAVKFIDNTLYFAEDDENLESD 36
|||||
DB 1 MAAEPEVDNCINFAVKFIDNTLYFAEDDENLESD 36

RESULT 2

Q9BG15 PRELIMINARY; PRT; 193 AA;
AC Q9BG15;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Interleukin-18.
GN ILI8.
OS Macaca mulatta (Rhesus macaque).

OS	Sus scrofa (Pig)
OC	Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID=9823;
	[1]
RN	SEQUENCE FROM N.A.
RP	TISSUE=LUNG;
RC	

Query Match 58.5%; Score 110; DB 11; Length 196;
Best Local Similarity 63.9%; Pred. No. 9:1e-08;

RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
RA Jags K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajadream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrall B.G.;
RT "the genome sequence of the food-borne pathogen *Campylobacter jejuni*
RT reveals hypervariable sequences";
RL Nature 403:665-668(2000).
DR "EMBL: AL139077; CAB73304.1; -
DR InterPro: IPR001261; ARGE-DAPE-CPG2.
DR Pfam: PF01546; Peptidase_M20.
DR TIGRFAMS: TIGR01246; daPE_prototeo.1.
DR PROSITE: PS00758; ARGE-DAPE-CPG2_1; UNKNOWN_1.
KW Complete proteome
SQ SEQUENCE 365 AA; 40457 MW; AE85159CDF09CB7E CRC64;
Query Match 28.2%; Score 53; DB 16; Length 365;
Best Local Similarity 36.0%; Pred. No. 22;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 5 PVEDNCINFVAMKFIDNTLYFAED 29
Db 18 PNDGALNFTAMELSDFAFFIEKE 42
RESULT 14
O9GV97 PRELIMINARY; PRT; 1039 AA.
AC O9GV97
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Plasma-membrane H+-ATPase.
GN PMAL
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Elmeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P-SPRAIN;
RX MEDLINE=21126593; PubMed=11223136;
RA Holpert M., Lueder C.G.K., Gross U., Bohne W.;
RT "Bradyzoite-specific expression of a P-type ATPase in *Toxoplasma*
RT gondii";
DR Moll. Biochem. Parasitol. 112:293-296(2001).
DR EMBL: AJ278874; CAC05676.1;
DR InterPro: IPR001757; ATPase_E1-E2.
DR InterPro: IPR004014; Cation_ATPase.
DR InterPro: IPR000454; H_gnase/hydrase.
DR Pfam: PF00690; Cation_ATPase_N; 1.
DR Pfam: PF00122; E1-E2_ATPase; 1.
DR Pfam: PF00702; Hydrolase; 1.
DR PRINTS: PR00119; CARATPASE.
DR PRINTS: PR00120; HATPASE.
DR PROSITE: PS00154; ATPASE_E1_E2; UNKNOWN_1.
SQ SEQUENCE 1039 AA; 115658 MW; DAA52C61B7FFAB14 CRC64;
Query Match 28.2%; Score 53; DB 5; Length 1039;
Best Local Similarity 43.5%; Pred. No. 62;
Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 12 NFVAMKFIDNTLYFAEDNLE 34
Db 895 NNASKVMQNTVHEERERNE 917
RESULT 15
O9DB53 PRELIMINARY; PRT; 149 AA.
ID O9DB53
AC Q9DB53

DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 1110008E19RIK protein.
GN 1110008E19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Yamada S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada S.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
DR EMBL: AK005215; BAB23888.1;
DR HSP; Q04760; IOP.
DR MGD: MGI:1913383; 1110008E19RIK.
DR InterPro: IPR004361; Glyoxalase_1.
DR InterPro: IPR004360; Gly-bleo_diox.
DR Pfam: PF00903; Glyoxalase; 1.
DR PRODOM: PD002334; Glyoxalase_1; 1.
DR TIGRFAMS: TIGR00068; glyox_I; 1.
DR PROSITE: PS00935; GLYOXALASE_1_2; 1.
SQ SEQUENCE 149 AA; 17036 MW; 5CAF060B831D1B82 CRC64;
Query Match 27.9%; Score 52.5; DB 11; Length 149;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 11; Conservative 6; Mismatches 2; Indels 3; Gaps 1;
QY 11 INFVAMKFIDNTLYFAEDDEN 32
Db 26 LDFFAMKF---SLYFLAYEDKN 44
Search completed: April 23, 2003; 08:18:14
Job time : 88 secs

Devil, S.
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FILE 'REGISTRY' ENTERED AT 10:29:52 ON 23 APR 2003
L1 15 S MAAEPVEDNCINFVAMKFIDNTLYFIAEDDENLESD/SQSP

FILE 'HCAPLUS' ENTERED AT 10:31:01 ON 23 APR 2003
L2 13 S L1

L2 ANSWER 1 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2003:55562 HCAPLUS

DOCUMENT NUMBER: 138:84318

TITLE: Generation and initial analysis of more than
15,000 full-length human and mouse cDNA
sequences

AUTHOR(S): Strausberg, Robert L.; Feingold, Elise A.;
Grouse, Lynette H.; Derge, Jeffery G.; Klausner,
Richard D.; Collins, Francis S.; Wagner, Lukas;
Shenmen, Carolyn M.; Schuler, Gregory D.;
Altschul, Stephen F.; Zeeberg, Barry; Buetow,
Kenneth H.; Schaefer, Carl F.; Bhat, Narayan K.;
Hopkins, Ralph F.; Jordan, Heather; Moore, Troy;
Max, Steve I.; Wang, Jun; Hsieh, Florence;
Diatchenko, Luda; Marusina, Kate; Farmer, Andrew
A.; Rubin, Gerald M.; Hong, Ling; Stapleton,
Mark; Soares, M. Bento; Bonaldo, Maria F.;
Casavant, Tom L.; Scheetz, Todd E.; Brownstein,
Michael J.; Usdin, Ted B.; Toshiyuki, Shiraki;
Carninci, Piero; Prange, Christa; Raha, Sam S.;
Loquellano, Naomi A.; Peters, Garrick J.;
Abramson, Rick D.; Mullahy, Sara J.; Bosak,
Stephanie A.; McEwan, Paul J.; McKernan, Kevin
J.; Malek, Joel A.; Gunaratne, Preethi H.;
Richards, Stephen; Worley, Kim C.; Hale, Sarah;
Garcia, Angela M.; Gay, Laura J.; Hulyk, Stephen
W.; Villalon, Debbie K.; Muzny, Donna M.;
Sodergren, Erica J.; Lu, Xiuhua; Gibbs, Richard
A.; Fahey, Jessica; Helton, Erin; Kettelman,
Mark; Madan, Anuradha; Rodrigues, Stephanie;
Sanchez, Amy; Whiting, Michelle; Madan, Anup;
Young, Alice C.; Shevchenko, Yuriy; Bouffard,
Gerard G.; Blakesley, Robert W.; Touchman,
Jeffrey W.; Green, Eric D.; Dickson, Mark C.;
Rodriguez, Alex C.; Grimwood, Jane; Schmutz,
Jeremy; Myers, Richard M.; Butterfield, Yaron S.
N.; Krzywinski, Martin I.; Skalska, Ursula;
Smailus, Duane E.; Schnerch, Angelique; Schein,
Jacqueline E.; Jones, Steven J. M.; Marra, Marco
A.

CORPORATE SOURCE: National Cancer Institute, NIH, Bethesda, MD,
20892-2580, USA

SOURCE: Proceedings of the National Academy of Sciences
of the United States of America (2002), 99(26),
16899-16903

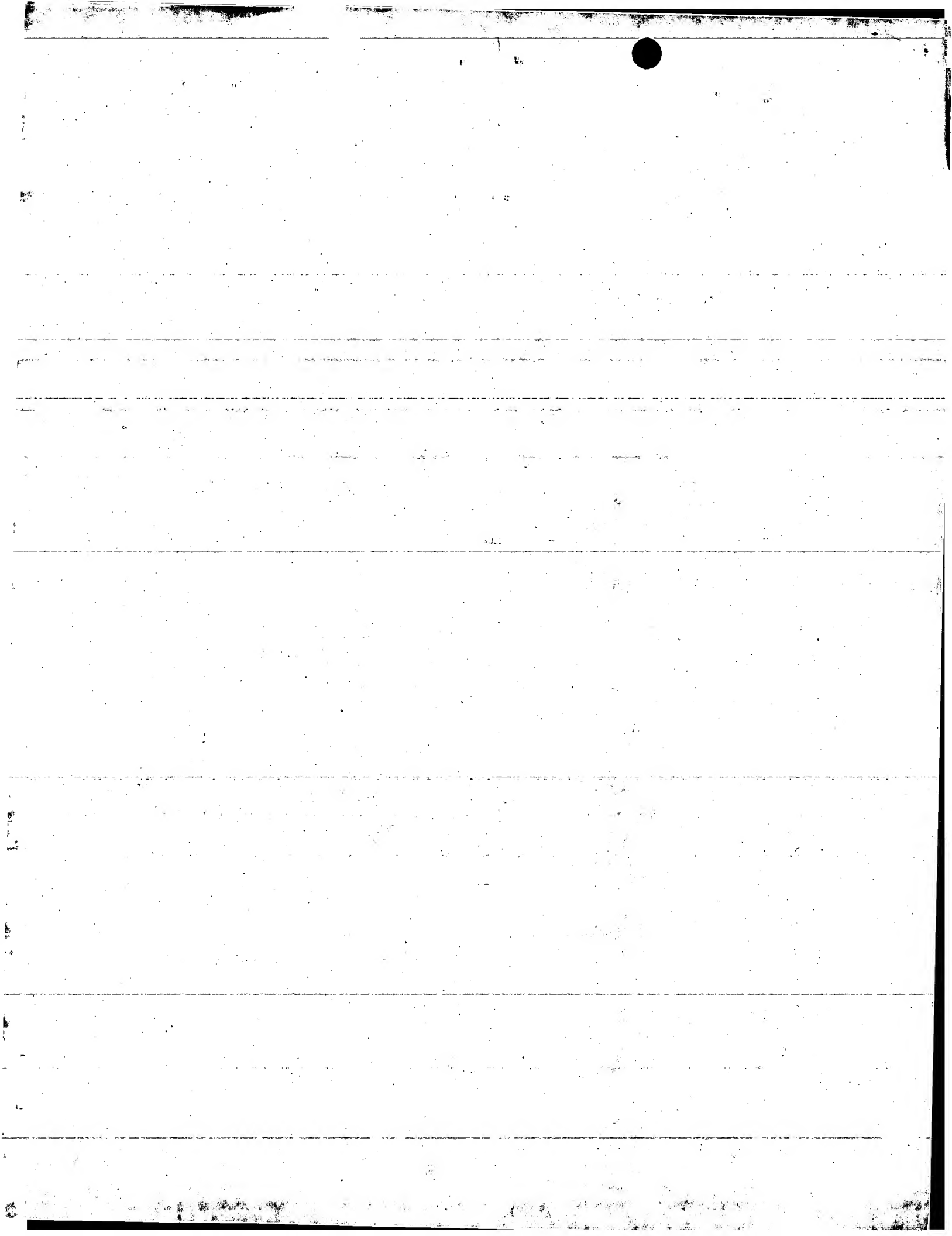
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The National Institutes of Health Mammalian Gene Collection (MGC)
Program is a multiinstitutional effort to identify and sequence a
cDNA clone contg. a complete ORF for each human and mouse gene.



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ESTs were generated from libraries enriched for full-length cDNAs and analyzed to identify candidate full-ORF clones, which then were sequenced to high accuracy. The MGC has currently sequenced and verified the full ORF for a nonredundant set of >9000 human and >6000 mouse genes. Candidate full-ORF clones for an addnl. 7800 human and 3500 mouse genes also have been identified. All MGC sequences and clones are available without restriction through public databases and clone distribution networks. [This abstr. record is one of eleven records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.]

IT 480762-83-2, GenBank AAH07007 480765-89-7

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; generation and initial anal. of more than 15,000 full-length human and mouse cDNA sequences)

L2 ANSWER 2 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:935747 HCAPLUS

DOCUMENT NUMBER: 136:68716

TITLE: Method for preparing a physiologically active IL-18 polypeptide

INVENTOR(S): Johanson, Kyung O.; Kirkpatrick, Robert B.; Shatzman, Allan R.; Ho, Yen Sen; McDevitt, Patrick

PATENT ASSIGNEE(S): Smithkline Beecham Corporation, USA

SOURCE: PCT Int. Appl., 64 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001098455	A2	20011227	WO 2001-US18804	20010611
WO 2001098455	A3	20020808		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
AU 2001080442	A5	20020102	AU 2001-80442	20010611
EP 1292697	A2	20030319	EP 2001-958830	20010611
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
PRIORITY APPLN. INFO.:	US 2000-211832P P 20000615			
	US 2000-224128P P 20000810			
	US 2001-264923P P 20010120			
	WO 2001-US18804 W 20010611			

AB A method for producing a physiol. active polypeptide, comprising contacting a precursor polypeptide with an activating enzyme, or

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co-expressing the polypeptide with an activating protease. The method is useful for inducing interferon .gamma. prodn. in immunocompetent cells, enhancing killing activity of NK cells, and promoting differentiation of naive CD4+ T cell into Th1 cells.

IT 383927-79-5P, Interleukin 18 (human precursor)
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; activation of IL-18 by contacting or co-expressing precursor IL-18 with an activating protease)

L2 ANSWER 3 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:693554 HCAPLUS
DOCUMENT NUMBER: 135:271914
TITLE: Treatment of allergies using an IL-18-antigen fusion protein
INVENTOR(S): Levy, Shoshana; Dekruffy, Rosemarie H.; Umetsu, Dale T.; Maecker, Holden
PATENT ASSIGNEE(S): Board of Trustees of the Leland Stanford Junior University, USA
SOURCE: PCT Int. Appl., 38 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001068896	A1	20010920	WO 2001-US6869	20010302
W: AU, CA, JP RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
US 2001044418	A1	20011122	US 2001-798075	20010302
PRIORITY APPLN. INFO.: US 2000-188311P P 20000310				
AB Allergic and other immune disorders assocd. with antigen specific T cells are treated by administering a vaccine comprising sequences of a fusion protein of IL-18 and antigen. The methods are particularly useful in decreasing an established antigen specific IgE immune response. Conditions of particular interest include asthma, allergic rhinitis, IgE-mediated anaphylactic reactions to insect stings, and other allergic conditions.				
IT 178234-94-1, Interleukin 18 (human precursor) RL: PRP (Properties) (unclaimed protein sequence; treatment of allergies using an IL-18-antigen fusion protein)				
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT				

L2 ANSWER 4 OF 13 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:376807 HCAPLUS
DOCUMENT NUMBER: 135:4468
TITLE: Antibody specific to interleukin 18 precursor
INVENTOR(S): Tohru, Kayano; Taniguchi, Mutsuko; Yamauchi, Hiroshi; Kurimoto, Masashi
PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo, Japan

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SOURCE: Eur. Pat. Appl., 27 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1101772	A1	20010523	EP 2000-310121	20001115
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2001204466	A2	20010731	JP 2000-349160	20001116
PRIORITY APPLN. INFO.: JP 1999-324860 A 19991116				
AB	Disclosed are an antibody specific to interleukin 18 (IL-18) precursor, prepn. processes therefor, and uses thereof. The antibody includes Igs in both forms of polyclonal and monoclonal antibodies which exhibits an immunoreactivity against IL-18 precursor at an intensity higher than against other substances. The antibody is useful in detection and purifn. of IL-18 precursor and in elimination and detoxification of the precursor accumulated in vivo. The detection method using the antibody is effective in qual. and quant. analyses for the precursor as well as in correction of imprecise results caused by assays using anti-IL-18 antibody which exhibits a cross reactivity against the precursor.			
IT	178254-43-8 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (amino acid sequence; antibody specific to interleukin 18 precursor for treating autoimmune disease)			
IT	341990-01-0 RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (antibody specific to interleukin 18 precursor for treating autoimmune disease)			

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 5 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1999:774182 HCAPLUS

DOCUMENT NUMBER: 132:277966

TITLE: Cloning and expression of precursor and mature human interleukin-18 in Escherichia coli

AUTHOR(S): Du, Yong; Wang, Tao; Du, Guixin; Xu, Jing; Hou, Lihua; Wang, Haitao

CORPORATE SOURCE: Department of Applied Molecular Biology, Beijing Institute of Microbiology and Epidemiology, Beijing, 100071, Peop. Rep. China

SOURCE: Mianyxue Zazhi (1999), 15(4), 226-228

CODEN: MIZAED; ISSN: 1000-8861

PUBLISHER: Mianyxue Zazhi Bianjibu

DOCUMENT TYPE: Journal

LANGUAGE: Chinese

AB The cDNAs encoding precursor and mature human interleukin-18 was amplified from total RNA of a hepatitis C virus carrier's peripheral blood mononuclear cells (PBMC) by RT-PCR resp. Two recombinant plasmids pQEIL18p and pQEIL18m were constructed by cloning cDNA of

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IL-18m into pQE-30 vector. The E. coli M15 harboring the two kinds of constructs expressed recombinant proteins with mol. wt. 24 KD and 19 KD, resp. by induction of IPTG. Both proteins were purified with Nickel chelate affinity chromatog. The recombinant mature IL-18 induced INF-.gamma. prodn. of Con A-stimulated PBMC.

IT 263886-60-8

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; cloning and expression of precursor and mature human interleukin-18 in Escherichia coli)

L2 ANSWER 6 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:133621 HCAPLUS

DOCUMENT NUMBER: 128:166370

TITLE: Preparation of an interferon-gamma inducing polypeptide

INVENTOR(S): Tanimoto, Tadao; Kurimoto, Masashi

PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku
Kenkyujo, Japan

SOURCE: Eur. Pat. Appl., 18 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 821005	A2	19980128	EP 1997-305376	19970718
EP 821005	A3	19991013		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 5891663	A	19990406	US 1997-896501	19970718
JP 10271998	A2	19981013	JP 1997-213885	19970725
PRIORITY APPLN. INFO.:			JP 1996-213267	19960725
			JP 1997-31474	19970131

AB A method for converting a precursor of a polypeptide that induces IFN-.gamma. prodn. in immunocompetent cells, characterized in that it comprises a step of contacting an interleukin-1.beta. converting enzyme with the precursor to convert it into an active polypeptide that induces IFN-.gamma. prodn. in immunocompetent cells. PRCHuGF contg. precursor polypeptide and pCDHICE encoding interleukin 1.beta.-converting enzyme were prepd., and active polypeptide contg. Tyr-Phe-Gly-Lys-Leu at the N-terminal region was purified for inducing prodn. of interferon .gamma..

IT 178234-94-1, Interleukin 18 (human) 202608-43-3

RL: PRP (Properties)

(amino acid sequence; prepn. of .gamma. interferon prodn.-inducing polypeptide and interleukin 1.beta.-converting enzyme)

IT 202538-32-7P

RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(prepn. of .gamma. interferon prodn.-inducing polypeptide and interleukin 1.beta.-converting enzyme)

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L2 ANSWER 7 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:133533 HCAPLUS

DOCUMENT NUMBER: 128:151108

TITLE: Enzyme which activates an interferon-.gamma.
inducing polypeptide

INVENTOR(S): Tanimoto, Tadao; Kurimoto, Masashi

PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku
Kenkyujo, Japan

SOURCE: Eur. Pat. Appl., 18 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 819757	A2	19980121	EP 1997-305377	19970718
EP 819757	A3	19991013		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 10080270	A2	19980331	JP 1997-156062	19970530
TW 480285	B	20020321	TW 1997-86110174	19970717
US 5879942	A	19990309	US 1997-896605	19970718
PRIORITY APPLN. INFO.:			JP 1996-207691	A 19960719
			JP 1997-156062	A 19970530

AB An enzyme or a protein is disclosed which converts a precursor of a polypeptide that induces IFN-.gamma. prodn. in an immunocompetent cell into the active form. The enzyme is produced from proliferating cells (THP-1, U-939, or HL-60 cells) and purified by (NH4)2SO4 pptn., and chromatog. on DEAD 5PW, S-Sepharose, Mono S, and Superdex 200 columns. The enzyme activates the INF-.gamma.-inducing precursor protein by cleavage of the bond between Asp36 and Tyr37, has a mol. wt. of about 25,000 Da and about 10,000 Da on SDS-PAGE, and is inhibited by iodoacetamide and Ac-YVAD-CHO. Partial amino acid sequences are provided for peptide fragments of the enzyme.

IT 178234-94-1, Interleukin 18 (human) 202538-32-7
202608-43-3

RL: BPR (Biological process); BSU (Biological study, unclassified);
BIOL (Biological study); PROC (Process)
(enzyme which activates an interferon-.gamma. inducing
polypeptide)

L2 ANSWER 8 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:116142 HCAPLUS

DOCUMENT NUMBER: 128:137190

TITLE: Genomic DNA encoding a polypeptide capable of
inducing the production of interferon-.gamma.

INVENTOR(S): Okura, Takanori; Torigoe, Kakuji; Kurimoto,
Masashi

PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku
Kenkyujo, Japan

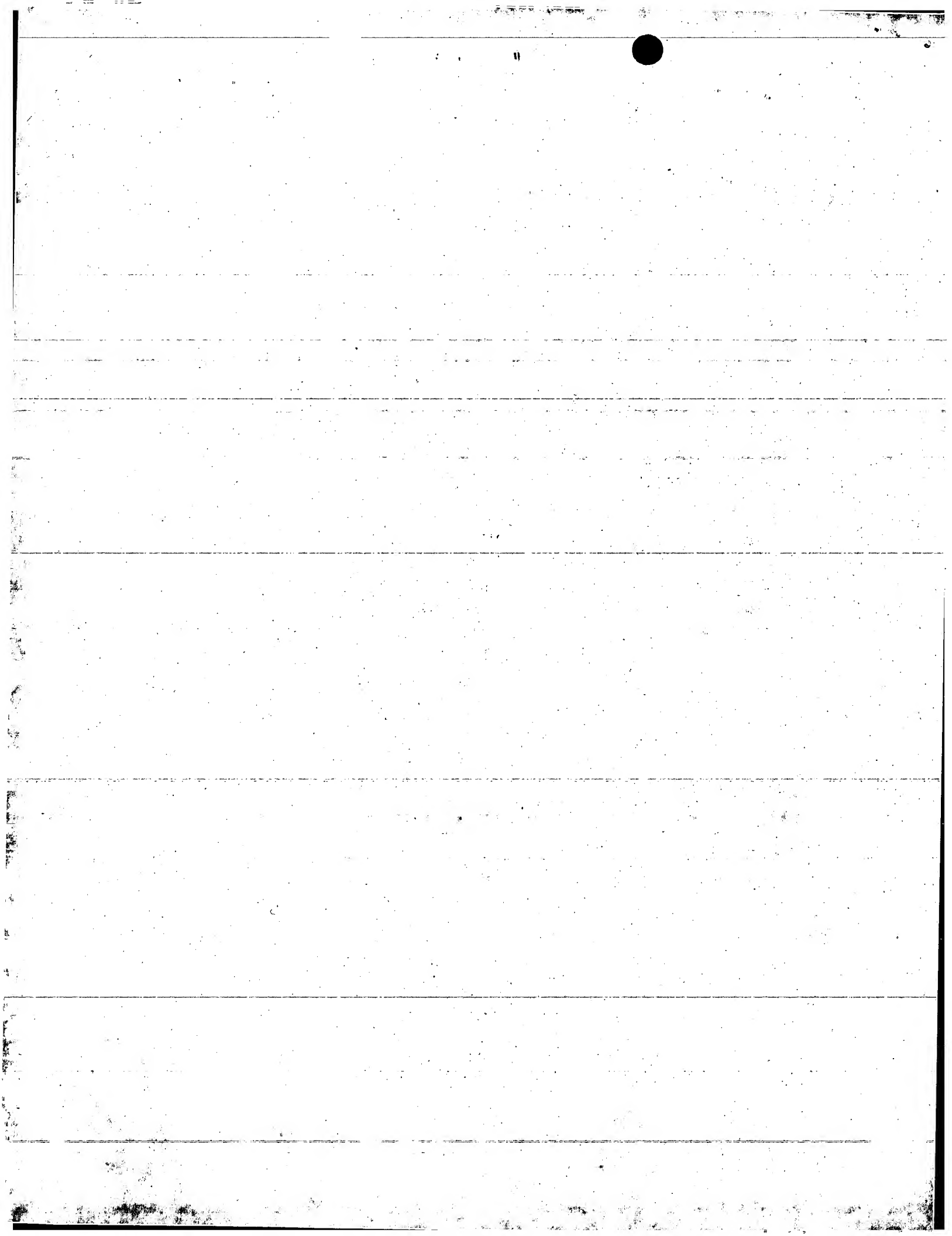
SOURCE: Eur. Pat. Appl., 74 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1



09/711896

PATENT INFORMATION:

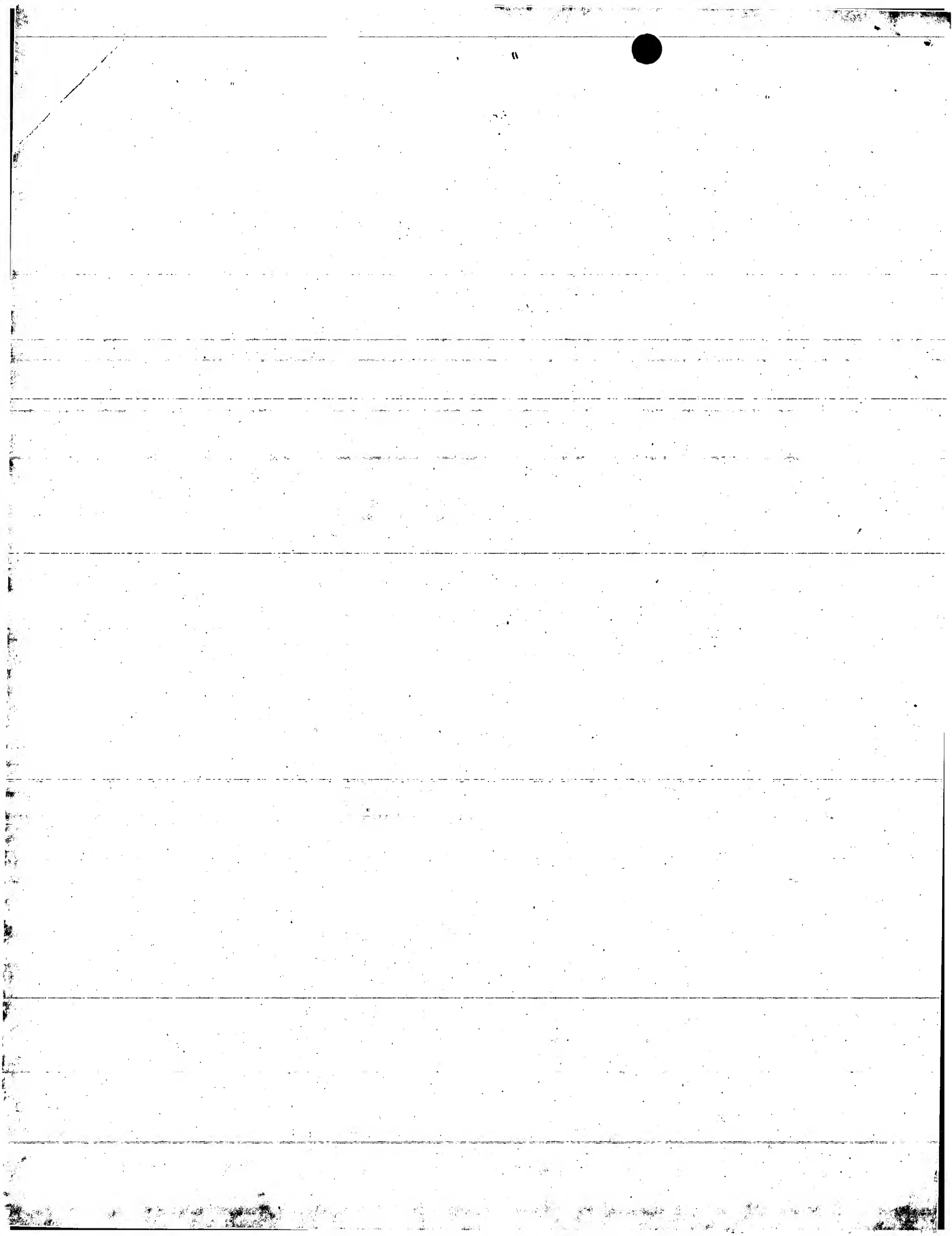
PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 816499	A2	19980107	EP 1997-304616	19970627
EP 816499	A3	19991027		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 10080288	A2	19980331	JP 1997-187418	19970627
US 6060283	A	20000509	US 1997-884324	19970627
PRIORITY APPLN. INFO.:			JP 1996-185305	19960627

AB Disclosed is a human genomic DNA encoding a polypeptide capable of inducing the prodn. of interferon-.gamma. by immunocompetent cells. The gene comprises at least 5 introns and 6 exons, and a sequence of 28,994 bp was detd. for the gene, including an extensive 5'-flanking region. The genomic DNA efficiently expresses the polypeptide with high biol. activities of such as inducing the prodn. of interferon-.gamma. by immunocompetent cells, enhancing killer cells' cytotoxicity and inducing killer cells' formation, when introduced into mammalian host cells. Recombinant plasmid vectors are constructed for expression of the polypeptide in Escherichia coli and CHO cells. The high biol. activities of the polypeptide facilitate its uses to treat and/or prevent malignant tumors, viral diseases, bacterial infectious diseases and immune diseases without serious side effects when administered to humans.

IT **178254-43-8P**
 RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (amino acid sequence; genomic DNA encoding a polypeptide capable of inducing the prodn. of interferon-.gamma.)

L2 ANSWER 9 OF 13 HCAPLUS COPYRIGHT 2003 ACS
 ACCESSION NUMBER: 1997:776271 HCAPLUS
 DOCUMENT NUMBER: 128:58316
 TITLE: Human interleukin-1.gamma. and antagonists thereof
 INVENTOR(S): Sana, Theodore R.; Timans, Jacqueline C.; Hardiman, Gerard T.; Kastelein, Robert A.; Bazan, J. Fernando
 PATENT ASSIGNEE(S): Schering Corporation, USA
 SOURCE: PCT Int. Appl., 62 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9744468	A1	19971127	WO 1997-US7282	19970516
W: AL, AM, AU, AZ, BA, BB, BG, BR, BY, CA, CN, CZ, EE, GE, HU, IL, IS, JP, KG, KR, KZ, LC, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, TT, UA, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				



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AU 9731166 A1 19971209 AU 1997-31166 19970516
EP 914453 A1 19990512 EP 1997-926391 19970516
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT,
IE, LT, LV, FI, RO

JP 2000511418 T2 20000905 JP 1997-542397 19970516
PRIORITY-APPLN. INFO.: US 1996-651998 A 19960520
WO 1997-US7282 W 19970516

AB Nucleic acids encoding human IL-1.gamma., and purified IL-1.gamma. proteins and fragments thereof are provided. Polyclonal and monoclonal antibodies, both anti-IL-1.gamma. antibodies and anti-idiotypic antibodies which may be agonists or antagonists of human IL-1.gamma., are also provided. Methods of using the compns. for both diagnostic and therapeutic utilities are also provided, together with antagonists and receptors of human IL-1.gamma..

IT 178234-94-1, Interleukin 18 (human)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; structure and antagonists of human interleukin-1.gamma.)

L2 ANSWER 10 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1997:689145 HCAPLUS

DOCUMENT NUMBER: 127:357917

TITLE: Involvement of caspase-1 and caspase-3 in the production and processing of mature human interleukin 18 in monocytic THP.1 cells

AUTHOR(S): Akita, Kenji; Ohtsuki, Takashi; Nukada, Yoshiyuki; Tanimoto, Tadao; Namba, Motoshi; Okura, Takanori; Takakura-Yamamoto, Rohko; Torigoe, Kakuji; Gu, Yong; Su, Michael S. -S.; Fujii, Mitsukiyo; Satoh-Itoh, Michiyo; Yamamoto, Kouzo; Kohno, Keizo; Ikeda, Masao; Kurimoto, Masashi

CORPORATE SOURCE: Fujisaki Institute, Hayashibara Biochemical Laboratories, Inc., Okayama, 702, Japan

SOURCE: Journal of Biological Chemistry (1997), 272(42), 26595-26603

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Recently, human interleukin 18 (hIL-18) cDNA was cloned, and the recombinant protein with a tentatively assigned N-terminal amino acid sequence was generated. However, natural hIL-18 has not yet been isolated, and its cellular processing is therefore still unclear. To clarify this, the authors purified natural hIL-18 from the cytosolic ext. of monocytic THP.1 cells. Natural hIL-18 exhibited a mol. mass of 18.2 kDa, and the N-terminal amino acid was Tyr37. Biol. activities of the purified protein were identical to those of recombinant hIL-18 with respect to the enhancement of natural killer cell cytotoxicity and interferon-.gamma. prodn. by human peripheral blood mononuclear cells. The authors also found two precursor hIL-18 (prohIL-18)-processing activities in the cytosol of THP.1 cells. These activities were blocked sep. by the caspase inhibitors Ac-YVAD-CHO and Ac-DEVD-CHO. Further analyses of the partially purified enzymes revealed that one is caspase-1, which cleaves prohIL-18 at the Asp36-Tyr37 site to generate the mature

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hIL-18, and the other is caspase-3, which cleaves both precursor and mature hIL-18 at Asp71-Ser72 and Asp76-Asn77 to generate biol. inactive products. Apparently, the prodn. and processing of natural hIL-18 are regulated by two processing enzymes, caspase-1 and caspase-3, in THP.1 cells.

IT 178234-94-1, Interleukin 18 (human)

RL: PRP (Properties)

(caspase-1 and caspase-3 in formation and processing of mature human interleukin 18 in monocytes)

L2 ANSWER 11 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1997:526678 HCAPLUS

DOCUMENT NUMBER: 127:148345

TITLE: Human interferon .gamma.-inducing factor-2 cDNA sequence, point mutation, and drug screening and disease diagnosis and therapy

INVENTOR(S): Coleman, Roger; Cocks, Benjamin Graeme; Hawkins, Phillip R.

PATENT ASSIGNEE(S): Incyte Pharmaceuticals, Inc., USA; Coleman, Roger; Cocks, Benjamin Graeme; Hawkins, Phillip R.

SOURCE: PCT Int. Appl., 59 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

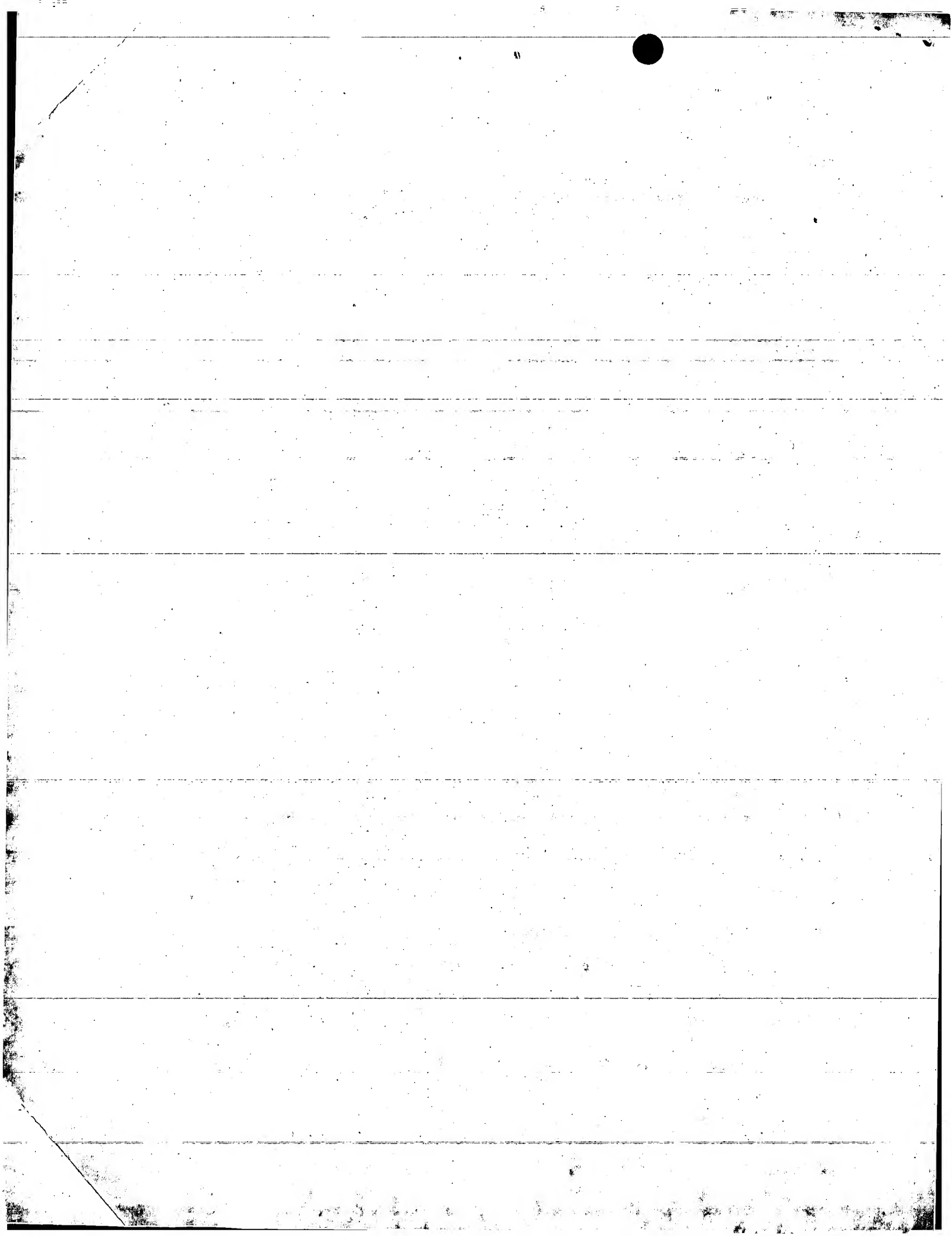
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9724441	A1	19970710	WO 1996-US20432	19961220
W: AT, AU, BA, BR, CA, CH, CN, DE, DK, ES, FI, GB, IL, JP, KR, LC, MX, NO, NZ, RU, SE, SG, US, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2238885	AA	19970710	CA 1996-2238885	19961220
AU 9713417	A1	19970728	AU 1997-13417	19961220
EP 870028	A1	19981014	EP 1996-944936	19961220
R: BE, DE, ES, FR, GB, IT, NL				
JP 2000502903	T2	20000314	JP 1997-524487	19961220
PRIORITY APPLN. INFO.:			US 1995-580667	19951229
			WO 1996-US20432	19961220

AB The present invention provides a polynucleotide (igif-2) which identifies and encodes a novel interferon .gamma.-inducing factor-2 (IGIF-2) which was expressed in adenoid, brain, kidney, liver, lung, skin, synovium, and T-lymphocytes. The present invention also provides for antisense mols. The invention further provides genetically engineered expression vectors and host cells for the prodn. of purified IGIF-2; antibodies, antagonists and inhibitors; and pharmaceutical compns. and methods of treatment based on the polypeptide, its antibodies, antagonists and inhibitors. The invention specifically provides for use of this polypeptide as therapeutic for immunocompromised individuals and as a pos. control in diagnostic assays for the detection of aberrant IGIF-2 expression or altered leukocyte or lymphocyte activity.

IT 178234-94-1P, Interleukin 18 (human) 193294-40-5P



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193294-41-6P

RL: ANT (Analyte); ARU (Analytical role, unclassified); BOC (Biological occurrence); BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); PROC (Process); USES (Uses)
(amino acid sequence; human interferon .gamma.-inducing factor-2 cDNA sequence, point mutation, and drug screening and disease diagnosis and therapy)

L2 ANSWER 12 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1996:397243 HCAPLUS

DOCUMENT NUMBER: 125:84660

TITLE: A peptide inducer of interferon .gamma. synthesis and antibodies against and their use in the treatment of interferon .gamma.-susceptible disease

INVENTOR(S): Ushio, Shimpei; Torigoe, Kakuji; Tanimoto, Tadao; Okamura, Haruki; Kunikata, Toshio; Taniguchi, Mutsuko; Kohno, Keizo; Fukuda, Shigeharu; Kurimoto, Masashi

PATENT ASSIGNEE(S): Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo, Japan

SOURCE: Eur. Pat. Appl., 48 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 712931	A2	19960522	EP 1995-308055	19951110
EP 712931	A3	19970326		
EP 712931	B1	20010214		
R: BE, CH, DE, DK, ES, FR, GB, IT, LI, NL, SE				
JP 08231598	A2	19960910	JP 1995-58240	19950223
JP 2952750	B2	19990927		
JP 08193098	A2	19960730	JP 1995-262062	19950918
JP 2724987	B2	19980309		
JP 10007699	A2	19980113	JP 1997-58547	19950918
TW 464656	B	20011121	TW 1995-84110504	19951004
CA 2162353	AA	19960516	CA 1995-2162353	19951107
EP 962531	A2	19991208	EP 1999-104104	19951110
EP 962531	A3	19991215		
R: BE, CH, DE, DK, ES, FR, GB, IT, LI, NL, SE				
ES 2156199	T3	20010616	ES 1995-308055	19951110
AU 9537796	A1	19960523	AU 1995-37796	19951113
AU 700948	B2	19990114		
US 6197297	B1	20010306	US 1995-558818	19951115
JP 09157180	A2	19970617	JP 1996-28722	19960124
US 6214584	B1	20010410	US 1997-832180	19970408
US 6268486	B1	20010731	US 1997-832177	19970408
US 6207641	B1	20010327	US 1997-974469	19971120
US 6509449	B1	20030121	US 2000-711899	20001115
PRIORITY APPLN. INFO.:				
				JP 1994-304203 A 19941115
				JP 1995-58240 A 19950223

Searcher : Shears 308-4994

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JP 1995-78357 A 19950310
JP 1995-262062 A 19950918
JP 1995-274988 A 19950929
JP 1995-279906 A 19951004
EP 1995-308055 A3 19951110
US 1995-558190 B2 19951115
US 1995-558191 A3 19951115
US 1995-558818 A3 19951115
US 1996-599879 B1 19960214

AB A polypeptide of 18,500. \pm 3,000 Da by SDS-PAGE and a pI of 4.9. \pm 1.0 by chromatofocusing that strongly induces the IFN- γ prodn. by immunocompetent cells at low concns. and that does not cause serious side effects even when administered to human in a relatively high dose is described. The protein is readily prepd. by immune affinity chromatog. using a monoclonal antibody and can be incorporated into agents for treating and/or preventing malignant tumors, viral diseases, bacterial infectious diseases, and immune diseases.

IT 178254-43-8P

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)

(amino acid sequence; peptide inducers of interferon γ synthesis of human and mouse and antibodies against and their use in treatment of interferon γ -susceptible disease)

L2 ANSWER 13 OF 13 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1996:314489 HCAPLUS

DOCUMENT NUMBER: 125:55848

TITLE: Cloning of the cDNA for human IFN- γ -inducing factor, expression in Escherichia coli, and studies on the biologic activities of the protein

AUTHOR(S): Ushio, Shimpei; Namba, Motoshi; Okura, Takanori; Hattori, Kazuko; Nukada, Yoshiyuki; Akita, Kenji; Tanabe, Fujimi; Konishi, Kaori; Micallef, Mark; et al.

CORPORATE SOURCE: Fujisaki Inst., Hayashibara Biochem. Lab., Inc., Okayama, Japan

SOURCE: Journal of Immunology (1996), 156(11), 4274-4279
CODEN: JOIMA3; ISSN: 0022-1767

PUBLISHER: American Association of Immunologists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The authors have recently reported that a novel mol., murine IFN- γ -inducing factor (IGIF) produced by mouse liver cells, possesses potent biol. activities, including the induction of IFN- γ prodn. by spleen cells and the enhancement of NK cell cytotoxicity. In this paper, the authors report on the isolation of human IGIF cDNA clones from normal human liver cDNA libraries using murine IGIF cDNA as a probe. The amino acid sequence deduced from the human cDNA clones indicated a 193-amino acid precursor peptide and revealed 65% homol. with that of murine IGIF. The amino acid sequence of IGIF also included an IL-1 signature-like sequence. Subsequently, the cloned cDNA was expressed in Escherichia coli, and preliminary studies on the biol. activities of the recombinant

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protein were performed. The recombinant human IGIF induced IFN-.gamma. prodn. by mitogen-stimulated PBMC and enhanced NK cell cytotoxicity, in a manner similar to murine IGIF. In addn., recombinant human IGIF also augmented granulocyte-macrophage-CSF prodn. and decreased IL-10 prodn., but had no effect on IL-4 prodn. by Con A-stimulated PBMC. Based on these pleiotropic effects of IGIF, the authors propose that this novel cytokine be designated as IL-18.

IT 178234-94-1, Interleukin 18 (human)
RL: PRP (Properties)
(amino acid sequence; cloning of cDNA for human IFN-.gamma.-inducing factor, expression in Escherichia coli, and studies on biol. activities of protein)

E1 THROUGH E11 ASSIGNED

FILE 'REGISTRY' ENTERED AT 10:33:49 ON 23 APR 2003
L3 11 SEA FILE=REGISTRY ABB=ON PLU=ON (178234-94-1/BI OR
178254-43-8/BI OR 202538-32-7/BI OR 202608-43-3/BI OR
193294-40-5/BI OR 193294-41-6/BI OR 263886-60-8/BI OR
341990-01-0/BI OR 383927-79-5/BI OR 480762-83-2/BI OR
480765-89-7/BI)

L4 11 L3 AND L1

L4 ANSWER 1 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 480765-89-7 REGISTRY
CN Interleukin 18 (interferon-gamma-inducing factor) (human clone
MGC:12320 IMAGE:3681009) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAH07461
CN GenBank AAH07461 (Translated from: GenBank BC007461)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN
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51 LNDQVLFIDQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIIISFK EMNPPDNIKD TKSDIIFFQR SVPGHDKMKQ
151 FESSSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED
HITS AT: 1-36

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:84318

L4 ANSWER 2 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 480762-83-2 REGISTRY
CN GenBank AAH07007 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAH07007 (Translated from: GenBank BC007007)
CN Interleukin 18 (interferon-gamma-inducing factor) (human clone
MGC:12321 IMAGE:3686124)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

Searcher : Shears 308-4994

09/711896

=====

51 LNDQVLFDIQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDNKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:84318

L4 ANSWER 3 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 383927-79-5 REGISTRY
CN Interleukin 18 (human precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO0198455 SEQID: 1 claimed protein
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN
=====

51 LNDQVLFDIQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDNKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:68716

L4 ANSWER 4 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 341990-01-0 REGISTRY
CN L-Aspartic acid, L-methionyl-L-alanyl-L-alanyl-L-.alpha.-glutamyl-L-prolyl-L-valyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-asparaginyl-L-cysteinyl-L-isoleucyl-L-asparaginyl-L-phenylalanyl-L-valyl-L-alanyl-L-methionyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-.alpha.-aspartyl-L-asparaginyl-L-threonyl-L-leucyl-L-tyrosyl-L-phenylalanyl-L-isoleucyl-L-alanyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-.alpha.-glutamyl-L-asparaginyl-L-leucyl-L-.alpha.-glutamyl-L-seryl-(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: EP1101772 SEQID: 1 claimed protein
CI MAN
SQL 36

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESD
=====

HITS AT: 1-36

REFERENCE 1: 135:4468

L4 ANSWER 5 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 263886-60-8 REGISTRY
CN Interleukin 18 (human clone pQEIL18p precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF077611-derived protein GI 3348071
CI MAN
SQL 193

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SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN
=====

51 LNDQVLFDIQ GNRPLLEDMT DSDCRDNAPR TIFIIRMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ SED

HITS AT: 1-36

REFERENCE 1: 132:277966

L4 ANSWER 6 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 202608-43-3 REGISTRY
CN Proteinase, interleukin 1.beta. precursor [73-isoleucine] (human
clone pRCHuGF precursor) (9CI) (CA INDEX NAME)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN
=====

51 LNDQVLFDIQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISIL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

REFERENCE 1: 128:166370

REFERENCE 2: 128:151108

L4 ANSWER 7 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 202538-32-7 REGISTRY
CN L-Leucine, L-methionyl-L-alanyl-L-alanyl-L-.alpha.-glutamyl-L-prolyl-
L-valyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-asparaginyl-L-
cysteinyl-L-isoleucyl-L-asparaginyl-L-phenylalanyl-L-valyl-L-alanyl-
L-methionyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-.alpha.-aspartyl-L-
asparaginyl-L-threonyl-L-leucyl-L-tyrosyl-L-phenylalanyl-L-isoleucyl-
L-alanyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-
.alpha.-glutamyl-L-asparaginyl-L-leucyl-L-.alpha.-glutamyl-L-seryl-L-
.alpha.-aspartyl-L-tyrosyl-L-phenylalanylglycyl-L-lysyl- (9CI) (CA
INDEX NAME)
CI MAN
SQL 41

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK L
=====

HITS AT: 1-36

REFERENCE 1: 128:166370

REFERENCE 2: 128:151108

L4 ANSWER 8 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 193294-41-6 REGISTRY
CN Interferon .gamma.-inducing factor-2 (human large isoform) (9CI)
(CA INDEX NAME)
CI MAN
SQL 205

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

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=====

51	LNDQVLFDIQ	GNRPLFEDMT	DSDCRDNAPR	TIFIISMYKD	SQPRGMAVTI
101	SVKCEKISTL	SCENKIISFK	EMNPPDNIKD	TKSDIIFQOR	SVPGHDKMQ
151	FESSYEGYF	LACEKERDLF	KLILKKEDEL	GDRSIMFTVQ	NEDGKVMNL
201	FFAN				

HITS AT: 1-36

REFERENCE 1: 127:148345

L4 ANSWER 9 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 193294-40-5 REGISTRY
CN Interferon .gamma.-inducing factor-2 [140-arginine] (human short isoform) (9CI) (CA INDEX NAME)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

=====

51	LNDQVLFDIQ	GNRPLFEDMT	DSDCRDNAPR	TIFIISMYKD	SQPRGMAVTI
101	SVKCEKISTL	SCENKIISFK	EMNPPDNIKD	TKSDIIFQOI	SVPGHDKMQ
151	FESSYEGYF	LACEKERDLF	KLILKKEDEL	GDRSIMFTVQ	NED

HITS AT: 1-36

REFERENCE 1: 127:148345

L4 ANSWER 10 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 178254-43-8 REGISTRY
CN Protein (human clone pHIGIF interferon .gamma.-inducing precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3: PN: EP1101772 SEQID: 4 claimed protein
CN Interleukin 18 (human precursor)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

=====

51	LNDQVLFDIQ	GNRPLFEDMT	DSDCRDNAPR	TIFIISMYKD	SQPRGMAVTI
101	SVKCEKISXL	SCENKIISFK	EMNPPDNIKD	TKSDIIFQOR	SVPGHDKMQ
151	FESSYEGYF	LACEKERDLF	KLILKKEDEL	GDRSIMFTVQ	NED

HITS AT: 1-36

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:4468

REFERENCE 2: 128:137190

REFERENCE 3: 125:84660

L4 ANSWER 11 OF 11 REGISTRY COPYRIGHT 2003 ACS
RN 178234-94-1 REGISTRY
CN Interleukin 18 (human precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO0168896 SEQID: 1 unclaimed protein
CN Cytokine IGIF (human precursor)
CN Interferon .gamma.-inducing factor (human precursor)
CN Interferon .gamma.-inducing factor-2 (human short isoform precursor)

09/711896

CN Interleukin 18 (human monocyte precursor)
CI MAN
SQL 193

SEQ 1 MAAEPVEDNC INFVAMKFID NTLYFIAEDD ENLESDYFGK LESKLSVIRN

=====

51 LNDQVLFIDQ GNRPLFEDMT DSDCRDNAPR TIFIISMYKD SQPRGMAVTI
101 SVKCEKISTL SCENKIISFK EMNPPDNIKD TKSDIIFQOR SVPGHDKMQ
151 FESSSYEGYF LACEKERDLF KLILKKEDEL GDRSIMFTVQ NED

HITS AT: 1-36

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:271914

REFERENCE 2: 128:166370

REFERENCE 3: 128:151108

REFERENCE 4: 128:58316

REFERENCE 5: 127:357917

REFERENCE 6: 127:148345

REFERENCE 7: 125:55848

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